

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:08:23 ; Search time 872.437 Seconds  
(without alignments)  
10014.946 Million cell updates/sec

Title: US-10-713-381-1\_COPY\_1\_1311

Perfect score: 1311  
Sequence: 1 ccaatggtcctctatgaataa.....cgacatctatctcctgaac 1311

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq 21.\*

1: geneseqn1980s:\*  
2: geneseqn1980s:\*  
3: geneseqn2001s:\*  
4: geneseqn2001s:\*  
5: geneseqn2001s:\*  
6: geneseqn2002s:\*  
7: geneseqn2002s:\*  
8: geneseqn2003s:\*  
9: geneseqn2003s:\*  
10: geneseqn2003s:\*  
11: geneseqn2003s:\*  
12: geneseqn2004s:\*  
13: geneseqn2004s:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1311	100.0	1394	2	AAx07408 Zea mays
2	1311	100.0	1394	2	AAx07409 Zea mays
3	1311	100.0	1394	5	AAH76332 Zea mays M
4	1311	100.0	1394	5	AAH76333 Zea mays M
5	160.6	12.3	255	5	AAH76340 Zea mays M
6	146	11.1	158	5	AAH76344 Zea mays M
7	74	5.6	320	13	ADK48600 Plant ful
8	74	5.6	624	13	ADK48600 Plant ful
9	72.8	5.6	2445	13	ADK33444 Plant ful
10	71.8	5.5	928	13	ADK61650 Plant ful
11	71.8	5.5	2537	13	ADK61650 Plant ful
12	71.8	5.5	3607	13	ADK61114 Plant ful
13	70.2	5.4	883	13	ADK60218 Plant ful
14	70.2	5.4	13400	11	AAH15210 Human bre
15	69.8	5.3	13400	11	ACN85231 Breast ca
16	68.2	5.3	537	13	ADK04296 Corn FT h
17	68.4	5.2	1215	13	ADK09466 Plant ful
18	68.4	5.2	1093	14	ADK49916 Plant ful
19	67.8	5.2	928	13	ABH28609 Maize pol
					ADK34996 Plant ful

C	20	67.4	5.1	1260	13	ADK60038	Ad60038 Plant ful
	21	67.2	5.1	2232	13	ADK33787	AdK33787 Plant ful
	22	67.2	5.1	2249	13	ADK45524	AdK45524 Plant ful
	23	67.2	5.1	2657	2	AAZ10551	AAZ10551 DNA seqe
	24	66.4	5.1	6027	2	AAK58751	AAK58751 Maize dui
	25	66.4	5.1	6027	8	ABX09935	ABX09935 DNA encod
	26	66.4	5.1	6027	12	ADK12106	ADK12106 cDNAenco
	27	66.2	5.0	439	8	ABK35844	ABK35844 Bovine ES
	28	65.6	5.0	1376	13	ADK08353	ADK08353 Plant ful
	29	65.6	5.0	346	4	AAH82729	AAH82729 Human pol
	30	65.6	5.0	2274	13	ADK08210	ADK08210 Plant ful
	31	65.6	5.0	2274	13	ADK082057	ADK082057 Plant ful
	32	65.6	5.0	8056	8	ABZ10246	ABZ10246 Haematopu
	33	64.6	4.9	9859	13	ADK89714	ADK89714 Oligonuci
	34	64.4	4.9	8056	8	ABZ10246	ABZ10246 Oligonuci
	35	64	4.9	8056	8	ABZ10100	ABZ10100 Haematopo
	36	63.8	4.9	431	8	ABK44556	ABK44556 Bovine ES
	37	63.6	4.9	335913	5	AAH61371	AAH61371 Soybean 2
	38	63.6	4.9	335913	5	AAH61372	AAH61372 Soybean 2
	39	63.4	4.8	12968	4	AAK45494	AAK45494 Chemical1
	40	63.4	4.8	12968	4	AAK45494	AAK45494 Chemical1
	41	63.4	4.8	12968	4	AAK45494	AAK45494 Chemical1
	42	63.4	4.8	12968	4	AAK45494	AAK45494 Chemical1
	43	63.4	4.8	12968	6	ABK28424	ABK28424 DNA trans
	44	63.2	4.8	12968	6	ABK28424	ABK28424 DNA trans
	45	63	4.8	1340	14	ADZ71035	ADZ71035 Human chr
						ABH34113	ABH34113 Human chr

#### ALIGNMENTS

RESULT 1	AAx07408 standard, DNA, 1394 BP.
ID	AAx07408
XX	AAx07408
AC	AAx07408
XX	08-JUN-1999 (first entry)
XX	
DB	Zea mays Ma45 male tissue-preferred regulatory region.
XX	
KW	Ma45; male; tissue-preferred; regulatory region; plant cells;
KW	plant tissue; differentiated; maize; hybrid seed; fertility; ss.
XX	
OS	Zea mays.
XX	
FN	W09859061-AL.
XX	
PD	30-DEC-1998.
XX	
XX	19-JUN-1998; 98WC-US012895.
XX	
PR	23-JUN-1997; 97US-00860499.
XX	
PA	(PION-) PIONEER HI-BRED INT INC.
XX	
XX	Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL;
XX	WPI; 1999-105628/09.
XX	
PT	New nucleic acid encoding a Ma45 male tissue-preferred regulatory region
PT	- useful in mediating plant fertility, especially hybrid seed production.
PS	Claim 2; Page 22-23; 39pp; English.
CC	The sequence is that encoding an Ma45 male tissue-preferred regulatory
CC	region. It may be used in the construction of a vector for a method of
CC	producing exogenous genes conferring fertility, such as in hybrid seed
CC	production. In conferring fertility, a monocot/dicot plant is transformed
CC	with the exogenous nucleotide sequence (a male sterility gene, preferably
CC	Ma45), which encodes a product selected from auxins, rols and dipteria
CC	toxins. Hybrid seeds are produced by cross-pollinating maize male fertile

CC and infertile plants  
XX  
SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;

Query Match	100.0%	Score 1311	DB 2	Length 1394
Best Local Similarity	100.0%	Pred. No. 1.2e-269		
Matches 1311	0	Mismatches	0	Gaps 0

QY	1	CAAGAGTCTCTATGAAAAGAGAGTACATGCTATATCCGTTTCTTGAAGGCTC	60
Db	1	CAATGATCTCTATGAAAAGAGAGTACATGCTATATCCGTTTCTTGAAGGCTC	60
QY	61	CTTCTTCTGCTTATTACTGACTGAATCGGGGTTACAAAACTTCCAGGGTGCATGAT	120
Db	61	CTTCTTCTGCTTATTACTGACTGAATCGGGGTTACAAAACTTCCAGGGTGCATGAT	120
QY	121	CTGCATGTTCCATTTCTCCCACTCCGGCTTACAATTTCTTGATGTCGGTGTCCCAT	180
Db	121	CTGCATGTTCCATTTCTCCCACTCCGGCTTACAATTTCTTGATGTCGGTGTCCCAT	180
QY	181	CTGACCGAGGCCCATCAGACACCTTTGGGACACCCATCAAGGGCTTTGGATGGCCCA	240
Db	181	CTGACCGAGGCCCATCAGACACCTTTGGGACACCCATCAAGGGCTTTGGATGGCCCA	240
QY	241	CGAGACGTATCGGGCTGTGTGATCCAGGGGATATATGTCCCCCAATTCGTCACTATA	300
Db	241	CGAGACGTATCGGGCTGTGTGATCCAGGGGATATATGTCCCCCAATTCGTCACTATA	300
QY	301	TTATTAATCTTAAATATTAATTTTGGAAAAAATAAACAATTAATCTTATGTGTA	360
Db	301	TTATTAATCTTAAATATTAATTTTGGAAAAAATAAACAATTAATCTTATGTGTA	360
QY	361	GGGGCTCAGCATAGATTTTCGCTTGAAGGCCCAGAAATCGAGGACCAAGCATGTCTAGTG	420
Db	361	GGGGCTCAGCATAGATTTTCGCTTGAAGGCCCAGAAATCGAGGACCAAGCATGTCTAGTG	420
QY	421	TCCACTATTTGSCACTACCCAGAAACAAGTTTAAAAAATPAACAAAGTAATCACT	480
Db	421	TCCACTATTTGSCACTACCCAGAAACAAGTTTAAAAAATPAACAAAGTAATCACT	480
QY	481	CGAAAGCATCATGTAATGTTTAAAGAAACATCTATTAAACCAAGATCCCTTAAAAAA	540
Db	481	CGAAAGCATCATGTAATGTTTAAAGAAACATCTATTAAACCAAGATCCCTTAAAAAA	540
QY	541	CAAGCATATTTGAAAGAGACAAATATATGTTTACAGTTTACAAACATCTAAGAGCGACAA	600
Db	541	CAAGCATATTTGAAAGAGACAAATATATGTTTACAGTTTACAAACATCTAAGAGCGACAA	600
QY	601	TTATATCGAAAGGTAGCTATGACGTTCAAGTTTTCTTTTCATTCCTTGTAATTTGTT	660
Db	601	TTATATCGAAAGGTAGCTATGACGTTCAAGTTTTCTTTTCATTCCTTGTAATTTGTT	660
QY	661	ATTGTTTTTAATADACTATTTCTTCTTAACAATAGAGATTTTCTCCGATTTTATATA	720
Db	661	ATTGTTTTTAATADACTATTTCTTCTTAACAATAGAGATTTTCTCCGATTTTATATA	720
QY	721	ATGACTATAAGTCAATTTTATATATAGACAGCATGTCGTATGATTCGTTCAAAAATC	780
Db	721	ATGACTATAAGTCAATTTTATATATAGACAGCATGTCGTATGATTCGTTCAAAAATC	780
QY	781	TTTCTGATTTTTTAAAGACTAGTTGGCAACCCGTGTTCTTTCAAAGATTTGATTTT	840
Db	781	TTTCTGATTTTTTAAAGACTAGTTGGCAACCCGTGTTCTTTCAAAGATTTGATTTT	840
QY	841	TTCAAAAAAATTAAGTTATTTCTCTTAATTAATATAGAAAACTTGAAGAAAAATAGAGT	900
Db	841	TTCAAAAAAATTAAGTTATTTCTCTTAATTAATATAGAAAACTTGAAGAAAAATAGAGT	900
QY	901	TGCCAGACTAGCCCTAGATATGTTTCCCAATTAATTAACATCACTGTGATATATATTTG	960
Db	901	TGCCAGACTAGCCCTAGATATGTTTCCCAATTAATTAACATCACTGTGATATATATTTG	960
QY	961	GCGAGCCCATTAATTAATTTAAACCGAACTGAATTCGAGGAAACCAATCTGACTAT	1020

Db	961	GCACGCCCCANPAATTTATTTHAACGAAACTGAAATGTGACGAAACCAAAATCTGAGCTAT	1020
Qy	1021	TTCTCTGATTTAGTAAAAAGGAGAGAGAGAGAGAAATCAGTTTAAAGTCATTTGTCCTC	1080
Db	1021	TTCTCTGATTTAGTAAAAAGGAGAGAGAGAGAGAAATCAGTTTAAAGTCATTTGTCCTC	1080
Qy	1081	TGAGATGTGGGGTTTGGCAACGATAGACCCGTTAATATATAGCTATAGTGTCCTACGTCA	1140
Db	1081	TGAGATGTGGGGTTTGGCAACGATAGACCCGTTAATATAGCTATAGTGTCCTACGTCA	1140
Qy	1141	GGTTCCGACGCTCTCGTGTCACTCCACATGGCATATACATGCTTTGTCAACCGTTGCTC	1200
Db	1141	GGTTCCGACGCTCTCGTGTCACTCCACATGGCATATACATGCTTTGTCAACCGTTGCTC	1200
Qy	1201	TTGTTCATCGTCCAAAGCCTTGCTATTTCTGAAACCAAGAGATACCTATCTCCCAAACAAT	1260
Db	1201	TTGTTCATCGTCCAAAGCCTTGCTATTTCTGAAACCAAGAGATACCTATCTCCCAAACAAT	1260
Qy	1261	CCATCTTACTCATGCAACTTCATGCAAAACAGCAGCATATGTTTCCCTGAAC	1311
Db	1261	CCATCTTACTCATGCAACTTCATGCAAAACAGCAGCATATGTTTCCCTGAAC	1311

## RESULT 2

ID AAX07409 standard; DNA; 1394 BP.

AC AAX07409 ;

DT 08-JUN-1999 (first entry)

**DE** Zea mays M845 male tissue-preferred regulatory region

KW MS45; male; tissue-preferred; regulatory region; plant cells;

XX

[illegible]

XX

XX

XX  
XX  
2  
THU 1003  
00776  
00000000

[illegible]

XX  
XX

XX  
WPT - 1000 10EC30/00  
DT

XX  
XX

PT - useful in mediating plant fertility, especially hybrid seed production.

PS Claim 3; Page 23-24; 39pp; English.

CC The sequence is that encoding an M845 male tissue-preferred regulatory

CC producing exogenous genes in a male tissue-preferred manner, which is

CC production. In conferring fertility, a monocot/dicot plant is transformed with the necessary nucleic acids necessary for male sterility gene expression.

CC Ms45), which encodes a product selected from auxins, rolB and diptheria

CC and infertile plants

**Sequence** 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;

Query Match	100.0%	Score 1311	DB 24	Length 1394
Best Local Similarity	100.0%	Pred. No. 126-259		
Matches 1311, Conservative	0	Mismatches	0	Gaps 0

QY 1 CCATGGTGTCTATGAGAAAAAGATGATCAATGTGTCTATATCCGTTTGTAGGATCC 60  
 Db 1 CCATGGTGTCTATGAGAAAAAGATGATCAATGTGTCTATATCCGTTTGTAGGATCC 60  
 QY 61 CTCTCTGCGCTTATTAAGTAAATGCGGGTTACAAAACTTTCAGCGGTGCAAT 120  
 Db 61 CTCTCTGCGCTTATTAAGTAAATGCGGGTTACAAAACTTTCAGCGGTGCAAT 120  
 QY 121 CTGCAATGTCACATCTCCACCTGCGTTGCAATTTCTTGATGTGGTGTTCAT 180  
 Db 121 CTGCAATGTCACATCTCCACCTGCGTTGCAATTTCTTGATGTGGTGTTCAT 180  
 QY 181 CTGACCGAGGCGCATGAGACATCTTGGGACACCATCAAGGCGCTTGGATGGCCA 240  
 Db 181 CTGACCGAGGCGCATGAGACATCTTGGGACACCATCAAGGCGCTTGGATGGCCA 240  
 QY 241 CGAGAGCTATCGGGTGGTGTATCGAGGGGATATATGTGCCCCCAATCTGACATTA 300  
 Db 241 CGAGAGCTATCGGGTGGTGTATCGAGGGGATATATGTGCCCCCAATCTGACATTA 300  
 QY 301 TTATATCTTTAGATATTTATTTTGAATAAATAAATAAATAAATAAATAAATAAATA 360  
 Db 301 TTATATCTTTAGATATTTATTTTGAATAAATAAATAAATAAATAAATAAATAAATA 360  
 QY 361 GGGGCTCAGACATATTTGCTTGAAGGCGCAAAATGCGAGACACGCAATGCTAG 420  
 Db 361 GGGGCTCAGACATATTTGCTTGAAGGCGCAAAATGCGAGACACGCAATGCTAG 420  
 QY 421 TCCACTATTTGGCACTACCCAGAACAAATTTAAATAAATAAATAAATAAATAAATA 480  
 Db 421 TCCACTATTTGGCACTACCCAGAACAAATTTAAATAAATAAATAAATAAATAAATA 480  
 QY 481 CGAAGCTATCATGTATATTTTAAAGAAACATCTATTAACCAAGTCTCTTAAATA 540  
 Db 481 CGAAGCTATCATGTATATTTTAAAGAAACATCTATTAACCAAGTCTCTTAAATA 540  
 QY 541 CAAGCATTTTGAAGAGACAAATTAATGTTACAGTTTCAAAATCTTAAGAGCACA 600  
 Db 541 CAAGCATTTTGAAGAGACAAATTAATGTTACAGTTTCAAAATCTTAAGAGCACA 600  
 QY 601 TTAATTCGAAGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 Db 601 TTAATTCGAAGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 QY 661 ATGTTTTTATACATTTCTCTCTAATGATGATGATGATGATGATGATGATGATG 720  
 Db 661 ATGTTTTTATACATTTCTCTCTAATGATGATGATGATGATGATGATGATGATG 720  
 QY 721 ATGACTATTAAGTCAATTTTATTAAGAGACGATGCTGATGCTGCTCAAAATC 780  
 Db 721 ATGACTATTAAGTCAATTTTATTAAGAGACGATGCTGATGCTGCTCAAAATC 780  
 QY 781 TTTCTGATTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTT 840  
 Db 781 TTTCTGATTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTT 840  
 QY 841 TTTCAAAAAAATAGTTATTTCTCTTATTAATGAAACCTTGAAGAAATAGT 900  
 Db 841 TTTCAAAAAAATAGTTATTTCTCTTATTAATGAAACCTTGAAGAAATAGT 900  
 QY 901 TGGCGACTAGCCCTAGATGATTTTCCAAATTAATCAATCTGATATTAATTTG 960  
 Db 901 TGGCGACTAGCCCTAGATGATTTTCCAAATTAATCAATCTGATATTAATTTG 960  
 QY 961 GCGAGCCCAATTAATTAATTAACCAAACTGAATGAGCGAAACCAATCTGACAT 1020  
 Db 961 GCGAGCCCAATTAATTAATTAACCAAACTGAATGAGCGAAACCAATCTGACAT 1020  
 QY 1021 TTCTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080  
 Db 1021 TTCTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080

QY 1081 TGAAGATGCGGTTTGGCAACATAGCCACCGTATATAGCTATAGGTGCTTACTCA 1140  
 Db 1081 TGAAGATGCGGTTTGGCAACATAGCCACCGTATATAGCTATAGGTGCTTACTCA 1140  
 QY 1141 GGTTCGGAGAGCTCTCGTGCATCTCAATGACATGACATGATGCTTGTAAACGTTGCTC 1200  
 Db 1141 GGTTCGGAGAGCTCTCGTGCATCTCAATGACATGACATGATGCTTGTAAACGTTGCTC 1200  
 QY 1201 TTGTTCAATGCTCAAGCTTGGCTTATTCGAACCAAGAGATACCTACTCCAAACAT 1260  
 Db 1201 TTGTTCAATGCTCAAGCTTGGCTTATTCGAACCAAGAGATACCTACTCCAAACAT 1260  
 QY 1261 CCATCTCTATGATGACATCTTCATGACAAACGACATATGTTTCTGTAC 1311  
 Db 1261 CCATCTCTATGATGACATCTTCATGACAAACGACATATGTTTCTGTAC 1311

RESULT 3  
 AAH76332  
 ID: AAH76332 standard; DNA; 1394 BP.  
 AAH76332;  
 29-OCT-2001 (first entry)  
 DE Z. maye M45 male tissue-preferred regulatory region encoding DNA.  
 KW M45; male tissue; regulatory region; transcription; male fertility;  
 KW hybrid seed; ds.  
 OS Zea mays.  
 NM W0200160997-A2.  
 PD 23-AUG-2001.  
 PF 13-FEB-2001; 2001WO-US004527.  
 PR 15-FEB-2000; 2000US-00504487.  
 PA (PION-) PIONEER HI-BRED INT. INC.  
 PI Albertsen MC, Fox TW, Garmaat CW, Huffman G, Kendall TL;  
 DR WPI; 2001-514772/56.  
 CC A male tissue-preferred regulatory region comprising nucleotide sequences  
 PT essential for initiating transcription of the M45 gene useful for  
 PT mediating fertility in a male plant.  
 PS Claim 4; Page 46; 50pp; English.  
 CC The invention provides a male tissue-preferred regulatory region (1)  
 CC comprising nucleotide sequences essential for initiating transcription of  
 CC the M45 gene. A method of mediating male fertility in a plant is  
 CC provided that involves introducing an expression vector comprising a  
 CC promoter operably linked to (1) into a plant where the exogenous gene  
 CC impacts male fertility of the plant and (1) controls expression of the  
 CC exogenous gene. A method of producing hybrid seeds is also provided. The  
 CC present sequence represents a nucleic acid sequence encoding an M45 male  
 CC tissue preferred regulatory region from Z. maye  
 SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1311; DB 5; Length 1394;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-269; Indels 0; Gaps 0;  
 Matches 1311; Conservative 0; Mismatches 0;

QY 1 CCATGGTGTCTATGAGAAAAAGATGATCAATGTGTCTATATCCGTTTGTAGGATCC 60  
 Db 1 CCATGGTGTCTATGAGAAAAAGATGATCAATGTGTCTATATCCGTTTGTAGGATCC 60  
 QY 61 CTCTCTGCGCTTATTAAGTAAATGCGGGTTACAAAACTTTCAGCGGTGCAAT 120  
 Db 61 CTCTCTGCGCTTATTAAGTAAATGCGGGTTACAAAACTTTCAGCGGTGCAAT 120  
 QY 121 CTGCAATGTCACATCTCCACCTGCGTTGCAATTTCTTGATGTGGTGTTCAT 180  
 Db 121 CTGCAATGTCACATCTCCACCTGCGTTGCAATTTCTTGATGTGGTGTTCAT 180  
 QY 181 CTGACCGAGGCGCATGAGACATCTTGGGACACCATCAAGGCGCTTGGATGGCCA 240  
 Db 181 CTGACCGAGGCGCATGAGACATCTTGGGACACCATCAAGGCGCTTGGATGGCCA 240  
 QY 241 CGAGAGCTATCGGGTGGTGTATCGAGGGGATATATGTGCCCCCAATCTGACATTA 300  
 Db 241 CGAGAGCTATCGGGTGGTGTATCGAGGGGATATATGTGCCCCCAATCTGACATTA 300  
 QY 301 TTATATCTTTAGATATTTATTTTGAATAAATAAATAAATAAATAAATAAATAAATA 360  
 Db 301 TTATATCTTTAGATATTTATTTTGAATAAATAAATAAATAAATAAATAAATAAATA 360  
 QY 361 GGGGCTCAGACATATTTGCTTGAAGGCGCAAAATGCGAGACACGCAATGCTAG 420  
 Db 361 GGGGCTCAGACATATTTGCTTGAAGGCGCAAAATGCGAGACACGCAATGCTAG 420  
 QY 421 TCCACTATTTGGCACTACCCAGAACAAATTTAAATAAATAAATAAATAAATAAATA 480  
 Db 421 TCCACTATTTGGCACTACCCAGAACAAATTTAAATAAATAAATAAATAAATAAATA 480  
 QY 481 CGAAGCTATCATGTATATTTTAAAGAAACATCTATTAACCAAGTCTCTTAAATA 540  
 Db 481 CGAAGCTATCATGTATATTTTAAAGAAACATCTATTAACCAAGTCTCTTAAATA 540  
 QY 541 CAAGCATTTTGAAGAGACAAATTAATGTTACAGTTTCAAAATCTTAAGAGCACA 600  
 Db 541 CAAGCATTTTGAAGAGACAAATTAATGTTACAGTTTCAAAATCTTAAGAGCACA 600  
 QY 601 TTAATTCGAAGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 Db 601 TTAATTCGAAGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 QY 661 ATGTTTTTATACATTTCTCTCTAATGATGATGATGATGATGATGATGATGATG 720  
 Db 661 ATGTTTTTATACATTTCTCTCTAATGATGATGATGATGATGATGATGATGATG 720  
 QY 721 ATGACTATTAAGTCAATTTTATTAAGAGACGATGCTGATGCTGCTCAAAATC 780  
 Db 721 ATGACTATTAAGTCAATTTTATTAAGAGACGATGCTGATGCTGCTCAAAATC 780  
 QY 781 TTTCTGATTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTT 840  
 Db 781 TTTCTGATTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTT 840  
 QY 841 TTTCAAAAAAATAGTTATTTCTCTTATTAATGAAACCTTGAAGAAATAGT 900  
 Db 841 TTTCAAAAAAATAGTTATTTCTCTTATTAATGAAACCTTGAAGAAATAGT 900  
 QY 901 TGGCGACTAGCCCTAGATGATTTTCCAAATTAATCAATCTGATATTAATTTG 960  
 Db 901 TGGCGACTAGCCCTAGATGATTTTCCAAATTAATCAATCTGATATTAATTTG 960  
 QY 961 GCGAGCCCAATTAATTAATTAACCAAACTGAATGAGCGAAACCAATCTGACAT 1020  
 Db 961 GCGAGCCCAATTAATTAATTAACCAAACTGAATGAGCGAAACCAATCTGACAT 1020  
 QY 1021 TTCTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080  
 Db 1021 TTCTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080

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|||
61 CTTCCTGCTCTTATTACTGACTGATCGGGGTACAAAAAATCTCCACGGGTGCATGAT 120
QY 121 CTCATGTCACATCTTCCACCTCGGGTGCACATTTCTTGAGTGCAGTGTCCCAT 180
Db 121 CTCATGTCACATCTTCCACCTCGGGTGCACATTTCTTGAGTGCAGTGTCCCAT 180
QY 181 CTGACCGAGGCCCATCAGACACCTTTGCGGACACCCATCAAGGGCTTTCCGATGGCCCA 240
Db 181 CTGACCGAGGCCCATCAGACACCTTTGCGGACACCCATCAAGGGCTTTCCGATGGCCCA 240
QY 241 CGAGACGTATGGGTGCTGGTGCATCGAGGGATATATGTCCCCCAATGCTACCTATA 300
Db 241 CGAGACGTATGGGTGCTGGTGCATCGAGGGATATATGTCCCCCAATGCTACCTATA 300
QY 301 TTATTAATCTTTAGATATTAATTTATTTTGGAAAAATTAACAACTTATACCTTTTGATA 360
Db 301 TTATTAATCTTTAGATATTAATTTATTTTGGAAAAATTAACAACTTATACCTTTTGATA 360
QY 361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCAGAAATCGAGACCAAGCCATGCTAGTG 420
Db 361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCAGAAATCGAGACCAAGCCATGCTAGTG 420
QY 421 TCCACTATTTGGCACTACCCAGAACAAATTTAAAAAATTAACAAAGTAACTTCCACT 480
Db 421 TCCACTATTTGGCACTACCCAGAACAAATTTAAAAAATTAACAAAGTAACTTCCACT 480
QY 481 CGAAGCATATGATGATTTTAAAGAAACATCTATTAACCAAGATCCTCTTAAAAAA 540
Db 481 CGAAGCATATGATGATTTTAAAGAAACATCTATTAACCAAGATCCTCTTAAAAAA 540
QY 541 CAAGCATATTTGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAGAGCGACAA 600
Db 541 CAAGCATATTTGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAGAGCGACAA 600
QY 601 TTATATGGAAGGTAGCTATGAGCTAGATTTTCTTTTCACTCTGTTATTTTGT 660
Db 601 TTATATGGAAGGTAGCTATGAGCTAGATTTTCTTTTCACTCTGTTATTTTGT 660
QY 661 ATGTTTTTATATATCATTTTCTCTCTACATATAGATTTTCTCGATTTTATATA 720
Db 661 ATGTTTTTATATATCATTTTCTCTCTACATATAGATTTTCTCGATTTTATATA 720
QY 721 ATGACTATTAAGTCAATTTTATATATAGACACGCTGTCGATGATCTGTTCAAAAATC 780
Db 721 ATGACTATTAAGTCAATTTTATATATAGACACGCTGTCGATGATCTGTTCAAAAATC 780
QY 781 TTTCTGATTTTATAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTT 840
Db 781 TTTCTGATTTTATAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTT 840
QY 841 TTCAAAAAAATTTGATTTTCTTTTATTAATAAAGAAACACTTGAAGAAATAGAGT 900
Db 841 TTCAAAAAAATTTGATTTTCTTTTATTAATAAAGAAACACTTGAAGAAATAGAGT 900
QY 901 TGCAGACTAGCCCTAGATGTTTTCCCATTAATTAATCACTGCTGTATATATTG 960
Db 901 TGCAGACTAGCCCTAGATGTTTTCCCATTAATTAATCACTGCTGTATATATTG 960
QY 961 GCCAGCCCATTAATTTATTAACCGAAATCGAAGGAAACCAATCTGAGCTAT 1020
Db 961 GCCAGCCCATTAATTTATTAACCGAAATCGAAGGAAACCAATCTGAGCTAT 1020
QY 1021 TTCTCTAGATTAAGTAAAGGAGAGAGAGAGAAATCAGTTTAAAGTATGTCCTC 1080
Db 1021 TTCTCTAGATTAAGTAAAGGAGAGAGAGAGAAATCAGTTTAAAGTATGTCCTC 1080
QY 1081 TGAAGTGTGCGGTTTGGCAACGATAGCAACGTTATCAATAGCTCAATAGTGTCTAC 1140
Db 1081 TGAAGTGTGCGGTTTGGCAACGATAGCAACGTTATCAATAGCTCAATAGTGTCTAC 1140
QY 1141 GGTTCGGACGCTCTGTGCTCATCTCAATGCGATCTACAGCTTGTTCACCGTTGCTC 1200

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Db 1141 GGTTCGGACGCTCTGTGCTCATCTCACATGCGATACATGCTTGTTCACCGTTGCTC 1200
QY 1201 TTGTTCCATGTCGCAACGCTTGGCTTATTTGAAACCAAGAGATACCTACTCCAAACAT 1260
Db 1201 TTGTTCCATGTCGCAACGCTTGGCTTATTTGAAACCAAGAGATACCTACTCCAAACAT 1260
QY 1261 CCATCTTACTGATGCAACTTCCATGCAACAGCAACATATGTTTCTGAAAC 1311
Db 1261 CCATCTTACTGATGCAACTTCCATGCAACAGCAACATATGTTTCTGAAAC 1311

RESULT 4
AAH76333
ID AAH76333 standard; DNA, 1394 BP.
AC AAH76333;
DT 29-OCT-2001 (first entry)
XX
XX
DE Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
KM Ms45; male tissue; regulatory region; transcription; male fertility;
KW hybrid seed; ds.
XX
OS Zea mays.
PN MO200160997-A2.
XX
PD 23-AUG-2001.
XX
FP 13-FEB-2001; 2001WO-US004527.
XX
PR 15-FEB-2000; 2000US-00504487.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
XX Albrechtsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX WPI; 2001-514772/56.
XX
PT A male tissue-preferred regulatory region comprising nucleotide sequences
PT essential for initiating transcription of the Ms45 gene useful for
PT mediating fertility in a male plant.
PS
PS Claim 4; Page 47; 50pp; English.
XX
CC The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription of
CC the Ms45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided. The
CC present sequence represents a nucleic acid sequence encoding an Ms45 male
CC -tissue preferred regulatory region from Z. mays
XX
SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;

Query Match 100.0%; Score 1311; DB 5; Length 1394;
Best Local Similarity 100.0%; Pred. NO. 1.2e-269; Indels 0; Gaps 0;
Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGTCGCTCTTATGAAAAAGATGATGATGATGCTATATCCGTTTCTTAAAGGTC 60
Db 1 CCATGTCGCTCTTATGAAAAAGATGATGATGATGCTATATCCGTTTCTTAAAGGTC 60
QY 61 CTTCCTTCTGCTTATTAAGTAAATCGGGTTTCAAAAACTTCCACGGGTGCATGAT 120
Db 61 CTTCCTTCTGCTTATTAAGTAAATCGGGTTTCAAAAACTTCCACGGGTGCATGAT 120
QY 121 CTCATGTCACATCTTCCACCTCGGGTGCACATTTCTTGAGTGCAGTGTCCCAT 180
Db 121 CTCATGTCACATCTTCCACCTCGGGTGCACATTTCTTGAGTGCAGTGTCCCAT 180

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QY 181 CTGACGAGGCCCATCAGACACCTTTGGGAGACCCCATCAGGCGCTTTGGAGTGGCA 240  
 DB 181 CTGACGAGGCCCATCAGACACCTTTGGGAGACCCCATCAGGCGCTTTGGAGTGGCA 240  
 QY 241 CGAGAGCTATCGGGTCGTGTGATCAGAGGGATATATGTCCCAATCTGACCTATA 300  
 DB 241 CGAGAGCTATCGGGTCGTGTGATCAGAGGGATATATGTCCCAATCTGACCTATA 300  
 QY 301 TTATATCTTTAGAT 360  
 DB 301 TTATATCTTTAGAT 360  
 QY 361 GGGGCTCAGCATATATTTGGCTTGGGCGCAAAATGCGAGACGACATGTCTAGTG 420  
 DB 361 GGGGCTCAGCATATATTTGGCTTGGGCGCAAAATGCGAGACGACATGTCTAGTG 420  
 QY 421 TCCATATGCGATCAGCCAGCAAGATTTAAAAAATTAACAAATTAATCACT 480  
 DB 421 TCCATATGCGATCAGCCAGCAAGATTTAAAAAATTAACAAATTAATCACT 480  
 QY 481 CGAAGCTATCATGATATTTTAAAGAAATCTATTAACAGATCTCTTAAAAA 540  
 DB 481 CGAAGCTATCATGATATTTTAAAGAAATCTATTAACAGATCTCTTAAAAA 540  
 QY 541 CAAGCATATTTGAAAAGACAAATATATGTTACATTAACAATCTTAAGGCGAGAA 600  
 DB 541 CAAGCATATTTGAAAAGACAAATATATGTTACATTAACAATCTTAAGGCGAGAA 600  
 QY 601 TTATATCGAAGGTAAGCTATGACGTTCAAGTTTTCTTTTCATTTGTTATTTGT 660  
 DB 601 TTATATCGAAGGTAAGCTATGACGTTCAAGTTTTCTTTTCATTTGTTATTTGT 660  
 QY 661 ATGTTTTTATATACATTTCTCTTCAATATAGATATTTCTCCATTTTATATA 720  
 DB 661 ATGTTTTTATATACATTTCTCTTCAATATAGATATTTCTCCATTTTATATA 720  
 QY 721 ATGCTATTAAGCATTTTATATTAAGAGCAGCATGCTGATCTCGTTCAAAAATC 780  
 DB 721 ATGCTATTAAGCATTTTATATTAAGAGCAGCATGCTGATCTCGTTCAAAAATC 780  
 QY 781 TTTCTGATTTTTTAAGCTATGTTGCAACCGCTTTCTTCAAGATTTTGAATTT 840  
 DB 781 TTTCTGATTTTTTAAGCTATGTTGCAACCGCTTTCTTCAAGATTTTGAATTT 840  
 QY 841 TTCAAAAAAATTAAGTATTTCTCTTATTAATTAAGAAACCTTGAAATATAGCT 900  
 DB 841 TTCAAAAAAATTAAGTATTTCTCTTATTAATTAAGAAACCTTGAAATATAGCT 900  
 QY 901 TGCAGACTAGCCCTAGATGTTTCCCAATTAATCAATCACTGTGATATATTTTG 960  
 DB 901 TGCAGACTAGCCCTAGATGTTTCCCAATTAATCAATCACTGTGATATATTTTG 960  
 QY 961 GCGAGCCCATTAATATTTTAAACGAACTGAATCGAGCGAAACCAATCTGAGCTAT 1020  
 DB 961 GCGAGCCCATTAATATTTTAAACGAACTGAATCGAGCGAAACCAATCTGAGCTAT 1020  
 QY 1021 TTCTCTAGATTAATTAATTAAGGAGAGAGAGAGAAATCAGTTTTAAGTCTTCC 1080  
 DB 1021 TTCTCTAGATTAATTAATTAAGGAGAGAGAGAGAAATCAGTTTTAAGTCTTCC 1080  
 QY 1081 TGAGATGTCGTTTGGCAAGATGCAACCGTATCATGATCATAGTTCCTAGCTCA 1140  
 DB 1081 TGAGATGTCGTTTGGCAAGATGCAACCGTATCATGATCATAGTTCCTAGCTCA 1140  
 QY 1141 GGTTCGAGAGCTCTGTCATCTCAGATGAGATCAATGCTTGTCAACGTTGCTC 1200  
 DB 1141 GGTTCGAGAGCTCTGTCATCTCAGATGAGATCAATGCTTGTCAACGTTGCTC 1200  
 QY 1201 TTGTTTCATGCTCAAGCTTGGCTATTTGAAACCAAGAGATCTACTCCAAACAT 1260  
 DB 1201 TTGTTTCATGCTCAAGCTTGGCTATTTGAAACCAAGAGATCTACTCCAAACAT 1260

QY 1261 CCATCTTACTGATGCAACTTCATGCAAAACAGCAATATGTTCTGATAC 1311  
 DB 1261 CCATCTTACTGATGCAACTTCATGCAAAACAGCAATATGTTCTGATAC 1311  
 RESULT 5  
 ID AAH76340  
 AC AAH76340; standard; DNA; 255 BP.  
 XX  
 AC AAH76340;  
 AC  
 XX 29-OCT-2001 (first entry)  
 XX  
 DE Z. maye M45 promoter fragment.  
 XX  
 XX M45; male tissue; regulatory region; transcription; male fertility;  
 XX hybrid seed; promoter; ds.  
 XX  
 OS Zea maye.  
 XX  
 PV NC0200160997-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PE 13-FEB-2001; 2001WO-US004527.  
 XX  
 PR 15-FEB-2000; 2000US-00504487.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Albetzen MC, Fox TW, Garnat CW, Huffman G, Kendall TL;  
 XX  
 DR WPI; 2001-514772/56.  
 XX  
 PT A male tissue-preferred regulatory region comprising nucleotide sequences  
 PT essential for initiating transcription of the M45 gene useful for  
 PT mediating fertility in a male plant.  
 PS  
 PS Example 5; Fig 8; 50pp; English.  
 CC The invention provides a male tissue-preferred regulatory region (I)  
 CC comprising nucleotide sequences essential for initiating transcription of  
 CC the M45 gene. A method of mediating male fertility in a plant is  
 CC provided that involves introducing an expression vector comprising a  
 CC promoter operably linked to (I) into a plant where the exogenous gene  
 CC impacts male fertility of the plant and (I) controls expression of the  
 CC exogenous gene. A method of producing hybrid seeds is also provided. The  
 CC present sequence represents a Z. maye M45 promoter fragment.  
 SX Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;  
 Query Match 12.3%; Score 160.6; DB 5; Length 255;  
 Best Local Similarity 97.6%; Pred. No. 1.5e-24;  
 Matches 163; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1145 CCGCAGCTCTCGCTGCTGATGATGAGATGATGATGATGATGATGATGATGATGAT 1204  
 DB 5 CCGCAGATCCGCTGCTGATGATGAGATGATGATGATGATGATGATGATGATGAT 64  
 QY 1205 TCCATGCTCAGACCTTGGCTTATGAAACCAAGAGATGATGATGATGATGATGAT 1264  
 DB 65 TCCATGCTCAGACCTTGGCTTATGAAACCAAGAGATGATGATGATGATGATGAT 124  
 QY 1265 CTTACTGATGCAACTTCATGCAAAACAGCAATATGTTCTGATAC 1311  
 DB 125 CTTACTGATGCAACTTCATGCAAAACAGCAATATGTTCTGATAC 124  
 RESULT 6  
 ID AAH76334  
 AC AAH76334; standard; DNA; 158 BP.  
 XX  
 AC AAH76334;

Query Match	Best Local Similarity	11.1%	Score 146	DB 5	Length 158
Matches 157	Conservative	0	Mismatches 0	Indels 1	Gaps 1
Qy	1155 CGTGCATCTGCATGCGCATCTACTACATGCTTGTTCACCGCTTCGTC-TTGTTCATCGTC	121			
Db	1 CGTGCATCTGCATGCGCATCTACTACATGCTTGTTCACCGCTTCGTC	60			
Qy	1214 CAAGCTTGCCCTATTTCTGAACCAAGAGATACCTACTCCCAAAACATCATCTTACTCAT	127			
Db	61 CAAGCTTGCCCTATTTCTGAACCAAGAGATACCTACTCCCAAAACATCATCTTACTCAT	120			
Qy	1274 GCAACTTCGATGCAACACGCGCATATGTCTTCTGAAAC	1311			
Db	121 GCAACTTCGATGCAACACGCGCATATGTCTTCTGAAAC	158			
RESULT 7					
ID	ADX48600	standard	CDNA	320 BP	
AC	ADX48600				
XX					
DT	21-APR-2005	(first entry)			
XX					
DE	Plant full length insert polynucleotide seqid 23340.				
XX					
KW	plant protectant; plant growth regulant; gene therapy; plant;				
KW	recombinant DNA construct; physical array; plant breeding marker;				
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;				

KM	extreme osmotic condition; pathogen tolerance; pest tolerance;
KM	growth rate; cell cycle pathway; disease resistance;
KM	galactomannan production; lignin production; plant growth regulator;
KM	yield; plant growth; plant development; seed oil; protein yield;
KM	protein content; gene; ss.
XX	
OS	Unidentified.
XX	
PN	US2004034888-A1.
PD	
XX	19-FEB-2004.
XX	
PF	28-APR-2003; 2003US-00425114.
XX	
PR	06-MAY-1999; 99US-00304517.
FR	05-NOV-2001; 2001US-00985678.
XX	
PA	(LIUJ/) LIU J.
PA	(ZHOU/) ZHOU Y.
PA	(KOVA/) KOVALIC D K.
PA	(SCRE/) SCREEN S E.
PA	(TABA/) TABASKA J E.
PA	(CAOY/) CAO Y.
XX	
PI	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX	
DR	WPI; 2004-180133/17.
XX	
PT	New recombinant DNA construct, useful for improving plant tolerance to
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT	pests, for conferring increased resistance to plant disease, or for
PT	improving yield.
XX	
PS	Claim 1; SEQ ID NO 23340; 15pp; English.
XX	
CC	The invention describes a recombinant DNA construct comprising a
CC	polynucleotide consisting of a sequence encoding an amino acid sequence
CC	available in electronic form from the US patent office at
CC	ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC	of the invention are also useful in physical arrays of molecules and as
CC	plant breeding markers. The recombinant DNA construct is useful for
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in
CC	plant cells by modification of the cell cycle pathway, for conferring
CC	increased resistance to plant disease, for producing galactomannan,
CC	lignin or plant growth regulators, for increasing the rate of homologous
CC	recombination in plants, for improving yield by modification of
CC	photoynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC	or by providing improved plant growth and development under at least one
CC	stress condition or for modifying seed oil or protein yield and/or
CC	content. This sequence represents a plant full length insert
CC	polynucleotide that can be used in the recombinant DNA construct of the
XX	invention.
XX	
SO	Sequence 320 BP; 89 A; 53 C; 66 G; 112 T; 0 U; 0 Other;
XX	
QY	Query Match 5.6%; Score 74; DB 13; Length 320;
QY	Best Local Similarity 73.1%; Pred. No. 4.6e-06;
QY	Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Db	
QY	791 TTTTAAAGCGTAGTTGGCAACCGCTTCTTTCAAGAATTTTGAATTTTCAAAAAA 850
Db	
QY	62 TTTTAAAGGCGTAGTTGGAAATTCATTTTTTTTCAAGAGATTTTATTTTCTTAAAGAA 121
Db	
QY	851 ATTAGTTATTTTCTCTTATATAAATGAAACAATTGAAATAATAGAGTTGCCAGACTA 910
Db	
QY	122 ATTAGTTATTTTCTTTGGAAGAAATGAAATTCCTTGGGAAATTAGAGTTCTTAAAGA 181
Db	
QY	911 GCCCTTAGAT 920
Db	
QY	182 GCCCTTAAT 191
Db	

RESULT 8  
AD33444  
ID AD33444 standard; cDNA; 624 BP.  
XX  
XX AD33444;  
AC  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 16264.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; 88.  
XX  
XX Unidentified.  
OS  
XX US200403488-A1.  
PN  
XX 19-FEB-2004.  
PD  
XX 28-APR-2003; 2003US-00425114.  
PF  
XX 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
XX (LITU//) LIU J.  
PA (ZHOU//) ZHOU Y.  
PA (KOV//) KOVALIC D K.  
PA (SCRE//) SCREEN S E.  
PA (TRBA//) TABASKA J E.  
PA (CAOV//) CAO Y.  
XX  
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
PI WPI: 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
XX Claim 1; SEQ ID NO 16264; 15bp; English.  
PS  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:200403488. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC lignin or plant growth regulators, for increasing the rate of uptake  
CC of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 624 BP; 170 A; 119 C; 146 G; 189 T; 0 U; 0 Other;  
Query Match 5.6%; Score 74; DB 13; Length 624;  
Best Local Similarity 73.1%; Pred. No. 5,4e-06;  
Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

XX 791 TTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTTTTCAGAAAAA 850  
XX |||||  
XX Db 374 TTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTTTTCAGAAAAA 433  
XX |||||  
XX Cy 851 ATTAGTTATTTTCTCTTAAATAAATAGAAAAACCTTGAATAAATAGAGTTCCAGACTA 910  
XX |||||  
XX Db 434 ATTAGTTATTTTCTCTTAAATAAATAGAAAAATTCCTTGGAAAAATTAGGTTCTTAAACA 493  
XX |||||  
XX Cy 911 GCCCTAGAAAT 920  
XX |||||  
XX Db 494 GCCCTTAAT 503  
XX |||||  
XX  
XX RESULT 9  
AD36150  
ID AD36150 standard; cDNA; 2445 BP.  
XX  
XX AD36150;  
AC  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 32493.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; 88.  
XX  
XX Unidentified.  
OS  
XX US200403488-A1.  
PN  
XX 19-FEB-2004.  
PD  
XX 28-APR-2003; 2003US-00425114.  
PF  
XX 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
XX (LITU//) LIU J.  
PA (ZHOU//) ZHOU Y.  
PA (KOV//) KOVALIC D K.  
PA (SCRE//) SCREEN S E.  
PA (TRBA//) TABASKA J E.  
PA (CAOV//) CAO Y.  
XX  
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
PI WPI: 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
XX Claim 1; SEQ ID NO 32493; 15bp; English.  
PS  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:200403488. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX Sequence 2445 BP; 666 A; 470 C; 513 G; 796 T; 0 U; 0 Other;  
Query March 5.5%; Score 72.8; DB 13; Length 2445;  
Best Local Similarity 73.6%; Pred. No. 1.4e-05;  
Matches 106; Conservative 0; Mismatches 37; Indels 1; Gaps 1;  
QY 792 TTTAAGAGCTAGTTGGCAACCTGTTCTT-TCAAGAAATTTGATTTTCAAAAAA 850  
DB 1623 TCTTAGGCTAGTTGAGAACCTTTTTCCTCCAAAGATTTTCATTTTCAAGAAA 1682  
QY 851 ATTAGTTATTTCTCTTTAATAAATAGAAAAACCTTAGAAAAATAGAGTCCAGACTA 910  
DB 1683 ATTAGTTATTTCTCTTTAATAAATAGAAAAACCTTAGAAAAATAGAGTTCAACTA 1742  
QY 911 GCCCTAGAAATGTTTCCCAATAA 934  
DB 1743 GCCCTAATGTTTTCATGAA 1766  
RESULT 10  
ADX34996/C  
ID ADX34996 standard; cDNA, 928 BP.  
AC ADX34996;  
DT 21-APR-2005 (first entry)  
XX Plant full length insert polynucleotide seqid 17816.  
DE  
XX plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
XX Unidentified.  
OS  
XX US2004034888-A1.  
PN  
XX 19-FEB-2004.  
PD  
XX 28-APR-2003; 2003US-00425114.  
PE  
XX 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
PR  
XX (LIU/J) LIU J.  
PA (ZHOU/Y) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/J) TABASKA J E.  
PA (CAO/Y) CAO Y.  
XX  
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
PI WPI; 2004-180133/17.  
DR  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
PS Claim 1; SEQ ID NO 17816; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docid=2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX Sequence 928 BP; 245 A; 209 C; 219 G; 255 T; 0 U; 0 Other;  
Query March 5.5%; Score 71.8; DB 13; Length 928;  
Best Local Similarity 78.0%; Pred. No. 1.8e-05;  
Matches 99; Conservative 0; Mismatches 27; Indels 1; Gaps 1;  
QY 790 TTTTAAGAGCTAGTTGGCAACCTGTTCTTTCAAGAAATTTTTCAAAAA 849  
DB 804 TTTTAAGAGCTAGTTGGCAACCTGTTCTTTCAAGAAATTTTTCAAAAA 746  
QY 850 AATTAGTTATTTCTCTTTAATAAATAGAAAAACCTTAGAAAAATAGAGTCCAGACT 909  
DB 745 AATTAGTTATTTCTCTTTAATAAATAGAAAAATAGCTTGAAAAATAGAGTTCCAAATT 686  
QY 910 AGCCCTA 916  
DB 685 ACCCTTA 679  
RESULT 11  
ADX61114  
ID ADX61114 standard; cDNA; 2537 BP.  
AC ADX61114;  
DT 21-APR-2005 (first entry)  
XX Plant full length insert polynucleotide seqid 31957.  
DE  
XX plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
XX Unidentified.  
OS  
XX US2004034888-A1.  
PN  
XX 19-FEB-2004.  
PD  
XX 28-APR-2003; 2003US-00425114.  
PE  
XX 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
PR  
XX (LIU/J) LIU J.  
PA (ZHOU/Y) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.

PA (TABAKA) TABASKA J E.  
PA (CAOY/) CAO Y.  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
XX Claim 1, SEQ ID NO 31957; 15pp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 2537 BP; 685 A; 484 C; 524 G; 844 T; 0 U; 0 Other;  
Query Match 5.5%; Score 71.8; DB 13; Length 2537;  
Best Local Similarity 73.4%; Pred. No. 2.2e-05;  
Matches 105; Conservative 0; Mismatches 37; Indels 1; Gaps 1;  
QY 792 TTTAAGAGCTAGTTGGCAACCTGTTCTTTCAGAAAGATTTGATTTTCAAAAAA 851  
DB 1799 TCTTAGGGCTAGTTGAGAACCT-TTTTCCCAAAAGATTTTCATTTTCAAGAAAA 1857  
QY 852 TTAGTTATTTTCTCTTTAATAATAGAAACACTTGAATAATAGAGTTCCAGACTG 911  
DB 1858 TTAGTTCAATTTTCTTGAAGAAATAGCAATCCCTTAAAAAATGTTTCAACTG 1917  
QY 912 CCTTAGATGTTTCCCAATAA 934  
DB 1918 CCTTAGATGTTTTCATGA 1940  
RESULT 12  
ADK60218 standard; cDNA; 3607 BP.  
ID ADK60218;  
XX  
XX ADK60218;  
XX  
XX 21-APR-2005 (first entry)  
XX  
XX Plant full length insert polynucleotide seqid 31061.  
XX  
XX plant protectant; plant growth regulator; gene therapy; plant;  
XX recombinant DNA construct; physical array; plant breeding marker;  
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
XX extreme osmotic condition; pathogen tolerance; pest tolerance;  
XX growth rate; cell cycle pathway; disease resistance;  
XX galactomannan production; lignin production; plant growth regulator;  
XX yield; plant growth; plant development; seed oil; protein yield;  
XX protein content; gene; ss.  
XX  
XX Unidentified.

PN US200403488-A1.  
XX  
XX PD 19-FEB-2004.  
XX  
XX PD 28-APR-2003; 2003US-00425114.  
XX  
XX PR 06-MAY-1999; 99US-00304517.  
XX  
XX PR 05-NOV-2001; 2001US-00985678.  
XX  
XX (LIU/) LIU J.  
XX (ZHOU/) ZHOU Y.  
XX (KOVA/) KOVALIC D K.  
XX (SCREEN/) SCREEN S E.  
XX (TABAKA/) TABASKA J E.  
XX (CAOY/) CAO Y.  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
XX Claim 1, SEQ ID NO 31061; 15pp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 3607 BP; 915 A; 695 C; 718 G; 1279 T; 0 U; 0 Other;  
Query Match 5.5%; Score 71.8; DB 13; Length 3607;  
Best Local Similarity 73.4%; Pred. No. 2.4e-05;  
Matches 105; Conservative 0; Mismatches 37; Indels 1; Gaps 1;  
QY 792 TTTAAGAGCTAGTTGGCAACCTGTTCTTTCAGAAAGATTTGATTTTCAAAAAA 851  
DB 2871 TCTTAGGGCTAGTTGAGAACCT-TTTTCCCAAAAGATTTTCATTTTCAAGAAAA 2929  
QY 852 TTAGTTATTTTCTCTTTAATAATAGAAACACTTGAATAATAGAGTTCCAGACTG 911  
DB 2930 TTAGTTCAATTTTCTTGAAGAAATAGCAATCCCTTAAAAAATGTTTCAACTG 2989  
QY 912 CCTTAGATGTTTCCCAATAA 934  
DB 2990 CCTTAGATGTTTTCATGA 3012  
RESULT 13  
AAL15210 standard; cDNA; 883 BP.  
ID AAL15210;  
XX  
XX AAL15210;  
XX  
XX 07-DEC-2001 (first entry)  
XX

DE Human breast cancer expressed polynucleotide 7667.  
XX  
XX Human; breast cancer; cell marker; cytostatic; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200151628-A2.  
XX  
PD 19-JUL-2001.  
XX  
XX 10-JAN-2001; 2001WO-US000798.  
XX  
XX 14-JAN-2000; 2000US-0176077P.  
XX  
XX 14-MAR-2000; 2000US-0189167P.  
XX  
XX 24-MAR-2000; 2000US-0192099P.  
XX  
XX 29-MAR-2000; 2000US-0193480P.  
XX  
XX 15-MAY-2000; 2000US-0205230P.  
XX  
XX 09-JUN-2000; 2000US-0211315P.  
XX  
XX 25-JUL-2000; 2000US-0220534P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
XX Lillie J, Xu Y, Wang Y, Steinmann K;  
XX  
XX WPI; 2001-451856/48.  
XX  
XX New peptide useful as a marker for the diagnosis of breast cancer.  
XX  
XX Claim 1; Page 1378; 3695pp; English.  
XX  
XX The invention relates to human breast cancer expressed polynucleotides  
XX (AAL07544-AAL26789) and methods of assessing whether a patient is  
XX afflicted with breast cancer by examining the correlation between the  
XX expression of certain markers and the cancerous state of breast cells.  
XX The polynucleotides and encoded polypeptides are potential markers for  
XX detecting, diagnosing, monitoring, characterizing, treating and  
XX potentially preventing breast cancer. The polynucleotides and encoded  
XX polypeptides are also useful for isolating compounds with cytostatic  
XX activity  
XX  
SQ Sequence 883 BP; 322 A; 18 C; 23 G; 396 T; 0 U; 124 Other;  
Query Match 5.4%; Score 70.2; DB 4; Length 883;  
Best Local Similarity 39.2%; Pred. No. 3.8e-05;  
Matches 237; Conservative 0; Mismatches 367; Indels 0; Gaps 0;  
QY 419 TGTCCACTATTGGGCACTACCCAGAACAGATTAAAAAATTAACCAAGTACTATCCCA 478  
DB 873 TGTNNANNANACCTANACCTTTAAANATNTNNANTTNAANNAAAAAAATATTTAAANN 814  
QY 479 CTCGAAAGCTATCATGTATGTTTAAAGAAACATCTATTAACACAGATCCTCTTAAA 538  
DB 813 TAAAAATTTTTTNNAAAACTAATTNTTAAANNATNAATNTTTTAAAAAANNAAAAA 754  
QY 539 AACAGCATATTTCGAAAGAGACAATATATGTACAGTTTCAAAACATCTAAGACGACA 598  
DB 753 TTAANNNTTTTNTAANTATTAACCAAAATTTTTTTTAAAAAATTTTTTAAAAAATT 694  
QY 599 AATATATATCGAAGGTAAGCATATGAGCTTCAGATTTTCTTTTCATCTCTGTTATTTG 658  
DB 693 AATATNTTAAATTTTTTTTAAATNAAAAAAATTTTAAATTAACCAANTNTTTTTT 634  
QY 659 TTATGTGTTTATATACATTTCTCTCTTACATATAGAGTGATTTTCTTCGATTTTATA 718  
DB 633 TTTTNTTNNATTAATAAAAAATTTTTTAAATTAATAAANNANNTTTTTTATNAANATTTAA 574  
QY 719 AATGACTATAAGCTATTTTATATTAAGAGACGACATGCTAGATTCCTGCAAAAA 778  
DB 573 AAAAAAANNTTTTTTTTTTAAANTTTAATTAATAAATTTTATTTNTTTTCTNAAAAANA 514  
QY 779 TCTTTCTGATTTTTTTAAGAGCTAGTTGGCAACCCCTGTTCTTCAAGAAATTTGATT 838  
DB 513 AAAAAAATTTTTTTTAAANTTTTAAAAAACCCTTAATTAATNAANNAATTTTTTTNNNT 454

QY 839 TTTTCAAAAAATTAAGTTATTTCTCTTATTAATAAGAAAAACCTAGAAAAATAGA 898  
DB 453 NNNATTTAAAAAATTTATTTTTTTTNTCTATTAATTAATAAANNAANNAATTAATAT 394  
QY 899 GTTGCCAGACTAGCCCTAGAAATGTTTCCCAATTAATTAACACTGCTATTAATATT 958  
DB 393 TTTTAAAAAATTAATTTATNTTATNTNAANNAANNAATTTTAAANNAANNAATTTTA 334  
QY 959 TGGCCAGCCCATTAATTTATTTAAGCGAATCTGAATCGAGGAAACCAATCTGAGCT 1018  
DB 333 NTTTAAATTAATTAATTAATTAATTAACATCTTTTATTTATTAATTAATAAAAAAAT 274  
QY 1019 ATTT 1022  
DB 273 NTTT 270  
RESULT 14  
ACN85231/C  
ID ACN85231 standard; DNA; 960 BP.  
XX  
XX ACN85231;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Breast cancer related marker, seq id 6381.  
XX  
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.  
XX  
XX Homo sapiens.  
XX  
XX US2003099974-A1.  
XX  
XX 29-MAY-2003.  
XX  
XX 18-JUL-2002; 2002US-00198846.  
XX  
XX 18-JUL-2001; 2001US-0306220P.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Lillie J, Xu Y, Wang Y, Steinmann K;  
XX  
XX WPI; 2003-787014/74.  
XX  
XX Novel isolated polypeptide associated with breast cancer, useful for  
XX detecting presence of polypeptide in sample, as a marker for breast  
XX cancer.  
XX  
XX Disclosure; SEQ ID NO 6381; 36pp; English.  
XX  
XX The invention relates to an isolated polypeptide (I) associated with  
XX breast cancer which is encoded by a nucleic acid molecule comprising a  
XX nucleotide sequence (S1). Further disclosed is an antibody that binds to  
XX the polypeptide of the invention. The activity of the polypeptide of the  
XX invention may be described as cytostatic. The antibody is useful for  
XX detecting the presence of (I) in a sample. Nucleic acid molecules of the  
XX invention are useful in the detection of breast tumours. (I) is useful as  
XX a marker for breast cancer and in breast cancer therapy. Sequences given  
XX in records ACN78851-ACN92934 represent nucleic acid markers associated  
XX with breast cancer. Note: The sequence listing does not form part of the  
XX specification but may be obtained in electronic format from the USPTO web  
XX site at [seqdata.uspto.gov/sequence.html?docId=2003099974](http://seqdata.uspto.gov/sequence.html?docId=2003099974)  
XX  
SQ Sequence 960 BP; 340 A; 33 C; 39 G; 421 T; 0 U; 127 Other;  
Query Match 5.4%; Score 70.2; DB 11; Length 960;  
Best Local Similarity 39.2%; Pred. No. 3.9e-05;  
Matches 237; Conservative 0; Mismatches 367; Indels 0; Gaps 0;  
QY 419 TGTCCACTATTGGGCACTACCCAGAACAGATTAAAAAATTAACCAAGTACTATCCCA 478

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Db 933 TGTNNANNACCTAACCCTTAANNNTNNNTNNTAANNAAAAATATTTAANN 874
Qy 479 CTCGAAGCATCATGTATAGTTTAAAGAAACATCTATTAAGACAGACCTCTTAAA 538
Db 873 TANAATTTTNNAAAACTATATTTNANNNTATNTATTTTNNAAAAAANNNAAAAA 814
Qy 539 AAGAGCATTTTCAGAAAGAGCAAAATTTATCTAGCTTACAAACATCTAAGACGACA 598
Db 813 TTAANNNTTTTNTAATTTATTAACCAAAATTTTNTTAAAAAATTTTAAAAAT 754
Qy 599 AATATATCGAAGAGTATGATGAGTCTGATTTTCTCTTCTCTCTCTCTCTCTCT 658
Db 753 AATATNTTAAATTTTNTTATTAATAAAAAAATTTTAAATTTTAAACAATNTTTT 694
Qy 659 TTAATGTTTATATATGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 718
Db 693 TTTTNTTNNATTAABAAAAATTTTAAATTAABAAAAAATTTTNTTAAATTTTAA 634
Qy 719 AATGACTATTAAGCATTTTATTAATTAAGACGACGATGCTGATTTCTCTGAAAA 778
Db 633 AAAAAAATTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 574
Qy 779 TCTTTCGATTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 838
Db 573 AAAAAAATTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNT 514
Qy 839 TTTTCAAAAAAATTTTATTTTCTCTTATTAATTAAGAAACATCTGAAAAATGA 898
Db 513 NNAATTTAAAAATTTTATTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNT 454
Qy 899 GTTGCAGCTAGCCCTGAAATGTTTCCCAATTAATTAATCAATCTGATTAATAT 958
Db 453 TTTNAAAAATTTTATTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 394
Qy 959 TGGCCAGCCCATTAATTTATTAACCGAACTGAATCGACGAAACCAATCTGACT 1018
Db 393 NTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 334
Qy 1019 ATTT 1022
Db 333 NTTT 330

RESULT 15
ID ADR04296 standard; DNA; 13400 BP.
AC ADR04296:
PT 04-NOV-2004 (first entry)
DE Corn FT homologue nucleotide sequence SEQ ID NO:63.
XX
XX flowering locus T gene; FT; terminal flower; TFL; Apetala3; Ap3; plant;
XX floral development; plant sterility; plant fertility; flowering time;
XX plant growth rate; inflorescence architecture; tissue culture morphology;
XX cell division; FT homologue; gene; ds.
XX
XX Zea mays.
XX
XX MO2004067723-A2.
XX
XX 12-AUG-2004.
XX
XX 29-JAN-2004; 2004WO-US002422.
XX
XX 30-JAN-2003; 2003US-00343477.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (DUPO-) DU PONT DE NEMOURS & CO E I.
XX
XX Danilevskaya O, Hermon P, Bruggemann E, Shirkoun D, Anan'ev E,
XX Rafalecki JA, Sakai H, Cahoon E, Cahoon R, Klein T,
PI

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XX WPI: 2004-58096/56.
XX
XX New polynucleotides, specifically nucleic acid fragments encoding
XX flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 (Ap3)
XX PT homologue, useful for floral development, e.g. engineering plant flowering
XX time.
XX
XX Claim 6, SEQ ID NO 63; 109bp; English.

```

The present invention describes an isolated polynucleotide comprising a first, second, third, fourth or fifth nucleotide sequence, or their complement encoding a polypeptide either having flowering locus T gene (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also described: (1) a vector comprising the polynucleotide; (2) a recombinant DNA construct comprising the polynucleotide; (3) transforming a cell by recombinant DNA construct; (4) producing a plant comprising transforming a plant cell with the polynucleotide, and regenerating a plant from the transformed plant cell; (5) a plant comprising the recombinant DNA construct; (6) a seed comprising the recombinant DNA construct; (7) an isolated polynucleotide comprising a first nucleotide sequence, where the first nucleotide sequence contains at least 30 nucleotides, and where the first nucleotide sequence is comprised by another polynucleotide, where the other polynucleotide includes the second, third, fourth, fifth or sixth nucleotide sequence; (9) an isolated polypeptide having FT or Ap3 homologue activity, as described above; and (10) isolating a polypeptide encoded by the polynucleotide comprising isolating the polypeptide from a cell containing a recombinant DNA construct comprising the polynucleotide operably linked to a regulatory sequence. The polynucleotides are useful for floral development, e.g. engineering plant sterility/fertility, and tissue culture morphology and the rate of cell division to enhance transformation. The present sequence represents an FT homologue nucleotide sequence from the present invention.

Sequence 13400 BP; 3962 A; 2948 C; 2695 G; 3795 T; 0 U; 0 Other;

Query Match 5.3%; Score 69.8; DB 13; Length 13400;  
Best Local Similarity 73.6%; Pred. No. 9e-05;  
Matches 89; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy 811 ACCCGTTCTTCAAGAAATTTGATTTTCAAAAAAATTTGTTATTTTCTCTTA 870
Db 8559 ACCATTTTATTTTCAAGGTTTATTTTATCAAGAAATTTGTTATTTTCTCTG 8618
Qy 871 TAAATGAAATCACTTGAAGAAATAGAGTTGCCAGATGACCTAGAAATGTTTCCCA 930
Db 8619 AAAAAATTAATTCATTAAGAAATGCGGTTGTCAAATGATGCTTATTTAGTTTCCAT 8678
Qy 931 T 931
Db 8679 T 8679

```

Search completed: March 5, 2006, 18:11:32  
Job time : 875.437 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:38:03 ; Search time 5721.35 Seconds  
(without alignments)  
13025.213 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1\_1311  
Perfect score: 1311  
Sequence: 1 ccatggtgcctcatgaaaa.....cgcacatattcttcgaac 1311

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5883141 segs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: 1: gb Da: \*  
2: gb In: \*  
3: gb Env: \*  
4: gb Om: \*  
5: gb Ov: \*  
6: gb Pat: \*  
7: gb Ph: \*  
8: gb Pr: \*  
9: gb Ro: \*  
10: gb Sts: \*  
11: gb Sy: \*  
12: gb Un: \*  
13: gb Vi: \*  
14: gb Hcg: \*  
15: gb Pl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1311	100.0	1394	6	BD062176 Male t18s
2	1311	100.0	1394	6	BD062177 Male t18s
3	1311	100.0	1394	6	AX224394 Sequence
4	1311	100.0	1394	6	AX224395 Sequence
5	1311	100.0	3343	15	AF360356 Zea mays
6	160.6	12.3	255	6	AX224396 Sequence
7	146	11.1	158	6	AX224396 Sequence
8	77.2	5.9	188283	14	AC155584 Zea mays
9	77.2	5.9	186199	14	AC147602 Zea mays
10	74.4	5.6	25769	2	AC117267 Dictyostel
11	72.4	5.5	172293	14	CR936840 Danio rer
12	72.4	5.5	201985	14	AC155379 Zea mays
13	71.6	5.4	713	2	AF034389 Plasmodi
14	71.2	5.4	3576	2	DDU86962 Dictyoste
15	71.2	5.4	317137	15	AY664413 Zea mays
16	70.8	5.4	149598	5	BX957346 Zebrafish
17	70.8	5.4	156452	14	AC155376 Zea mays
18	70.8	5.4	156452	14	AC155376 Zea mays

C 19	70.4	5.4	347582	2	PFMAL7P1	AL034557 Plasmodi
C 20	70.2	5.4	883	6	CQ422641	CQ422641 Sequence
C 21	70	5.3	241	10	BV119878	BV119878 PZA01377
C 22	70	5.3	247	10	BV119874	BV119874 PZA01377
C 23	70	5.3	248	10	BV119877	BV119877 PZA01377
C 24	69.8	5.3	13400	6	CO855052	CO855052 Sequence
C 25	69.6	5.3	134692	14	AC151050	AC151050 Zea mays
C 26	69.4	5.3	110000	15	CR382132_17	Continuation (18 o
C 27	69.2	5.3	112468	14	AC149836	AC149836 Zea mays
C 28	69.2	5.3	266544	2	AC116956	AC116956 Dictyoste
C 29	68.8	5.2	148120	14	AC155517	AC155517 Zea mays
C 30	68.8	5.2	186199	14	AC147602	AC147602 Zea mays
C 31	68.6	5.2	213	10	BV119875	BV119875 PZA01377
C 32	68.4	5.2	216	10	BV119871	BV119871 PZA01377
C 33	68.4	5.2	224	10	BV119882	BV119882 PZA01377
C 34	68.4	5.2	245	10	BV119881	BV119881 PZA01377
C 35	68.4	5.2	246	10	BV119869	BV119869 PZA01377
C 36	68.2	5.2	346296	15	AF090447	AF090447 Zea mays
C 37	68.2	5.2	1092	6	CS123057	CS123057 Sequence
C 38	68	5.2	110000	14	PFMAL7P1_02	Continuation (3 of
C 39	67.8	5.2	227495	14	AC148480	AC148480 Zea mays
C 40	67.6	5.2	351	10	BV110530	BV110530 PZA01059
C 41	67.6	5.2	110000	15	AY664419_2	Continuation (3 of
C 42	67.6	5.2	331039	2	AC116979	AC116979 Dictyoste
C 43	67.4	5.1	170	10	BV119873	BV119873 PZA01377
C 44	67.4	5.1	155263	14	BX927284	BX927284 Danio rer
C 45	67.2	5.1	155263	14	BX927284	BX927284 Danio rer

#### ALIGNMENTS

RESULT 1  
BD062176 1394 bp DNA linear PART 27-AUG-2002  
LOCUS Male tissue-preferred regulatory region and method of using same.  
DEFINITION BD062176.1 GI:22607781  
ACCESSION BD062176  
VERSION BD062176.1 GI:22607781  
KEYWORDS JP 2001520523-A/1.  
SOURCE Home sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and Kendall, T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL Patent: JP 2001520523-A 1 30-OCT-2001;  
COMMENT PIONEER HI BRED INTERNATIONAL INC  
PN JP 2001520523-A/1  
PD 30-OCT-2001 JP 1999504910  
PR 19-JUN-1998 JP 1999504910  
PR 23-JUN-1997 US 08/880499  
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAAT, GARY A HUFFMAN,  
PI TIMMY L KENDALL  
PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC  
PC C07K14/34, C1201/68,  
PC A01H5/00  
CC Strandedness: Single;  
CC Topology: Linear;  
CC key Location/Qualifiers

FEATURES  
source 1..1394  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

#### ORIGIN

Query Match 100.0%; Score 1311; DB 6; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 7.2e-228; Indels 0; Gaps 0;  
Matches 1311; Conservative 0; Mismatches 0;

```

Qy 1 CCATGAGTCTCTATGAAAAAGATGAGTACATGTCATATCCGTTTCTTAGGGTCC 60
Db 1 CCATGAGTCTCTATGAAAAAGATGAGTACATGTCATATCCGTTTCTTAGGGTCC 60
Qy 61 CTTCTTCTGCTTATATGCTGATGCGGTTTACAAAAAATTCCACGGGTGATGAT 120
Db 61 CTTCTTCTGCTTATATGCTGATGCGGTTTACAAAAAATTCCACGGGTGATGAT 120
Qy 121 CTCATGTTCCATCTTCCACCTCGCGTTGACATTTCTTGAGATGCGGTGTTCCAT 180
Db 121 CTCATGTTCCATCTTCCACCTCGCGTTGACATTTCTTGAGATGCGGTGTTCCAT 180
Qy 181 CTGACCGAGGCCCATCAGACACCTTTGCGGACACCCCATCAAGGGCTTTGCGATGCCA 240
Db 181 CTGACCGAGGCCCATCAGACACCTTTGCGGACACCCCATCAAGGGCTTTGCGATGCCA 240
Qy 241 CGAAGCGATGCGGTGCGTGTGATCCAGGGATATATGTCCTCCACATTCGTCACCTATA 300
Db 241 CGAAGCGATGCGGTGCGTGTGATCCAGGGATATATGTCCTCCACATTCGTCACCTATA 300
Qy 301 TTATATATCTTATGATATTTATTTTGGAAAAATACAACTTATACCTTTTGTGTA 360
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Qy 361 GGGCCTCAGCATATGTTTGGCTTAGGGCCAGAAATCGAGACACACCATGTCATG 420
Db 361 GGGCCTCAGCATATGTTTGGCTTAGGGCCAGAAATCGAGACACACCATGTCATG 420
Qy 421 TCCATATTTGGCATCACCAGAACAAATTTTAAAAAATACAAAGTATATCCACT 480
Db 421 TCCATATTTGGCATCACCAGAACAAATTTTAAAAAATACAAAGTATATCCACT 480
Qy 481 CGAAGCGATGATGATGTTTAAAGAAACATCTTATAAACAGATCCTTTAAAAA 540
Db 481 CGAAGCGATGATGATGTTTAAAGAAACATCTTATAAACAGATCCTTTAAAAA 540
Qy 541 CAAGCATATTTGAAAGAGACAAATTTATGATTTTACAAATCTTAAAGCGACAA 600
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Qy 601 TTAATATCGAAGGTAAGCTATGACGTTTCTTTTCTTCTTCTTCTTCTTCTTCTT 660
Db 601 TTAATATCGAAGGTAAGCTATGACGTTTCTTTTCTTCTTCTTCTTCTTCTTCTT 660
Qy 661 ATTGTTTTATATACATTTTCTTCTTACATAGATGATTTCTTCCGATTTTATAA 720
Db 661 ATTGTTTTATATACATTTTCTTCTTACATAGATGATTTCTTCCGATTTTATAA 720
Qy 721 ATGACTATTAAGTCAATTTTATATTAAGACAGCATGTCGATGATTTCTGTTCAAAATC 780
Db 721 ATGACTATTAAGTCAATTTTATATTAAGACAGCATGTCGATGATTTCTGTTCAAAATC 780
Qy 781 TTTCTGATTTTATTAAGCTTGTGGCAACCTGTTCTTCAAAATTTTGAATTT 840
Db 781 TTTCTGATTTTATTAAGCTTGTGGCAACCTGTTCTTCAAAATTTTGAATTT 840
Qy 841 TTCAAAAAATTAATTTTCTTCTTATTAATAGAAACACTTGAATAATAGAT 900
Db 841 TTCAAAAAATTAATTTTCTTCTTATTAATAGAAACACTTGAATAATAGAT 900
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Db 901 TCCGAGCTAGCCCTAGAAATGTTTCCCAATTAATCAATCATGCTGATATATTTG 960
Qy 961 GCGAGCCCATTAATTTTAAACCGAAATCGAGCGAAACCAATCTGAGCTAT 1020
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Qy 1021 TTCTTAGATTAATTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 TTCTTAGATTAATTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy 1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAAATCATAGCTCATAGGCTTACGTCA 1140

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Db 1141 GGTTCGAGAGCTCTGCTGATCATCATGATGATCATATGCTTGTCAACCGTTGTC 1200
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Db 1201 TTGTTCCATGCTTCCAGACCTTGCCTATTTCTGAAACCAAGAGATACCTACCCAAACAT 1260
Qy 1261 CCATCTTACTCATGCACTTCCATGCAACGACGACATATGTTCTCGAAC 1311
Db 1261 CCATCTTACTCATGCACTTCCATGCAACGACGACATATGTTCTCGAAC 1311

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## RESULT 2

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BD062177 1394 bp DNA linear PAT 27-AUG-2002
LOCUS Male tissue-preferred regulatory region and method of using same.
DEFINITION BD062177
ACCESSION BD062177.1 GI:22607782
VERSION JP 2001520523-A/2.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1394)
AUTHORS Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and
Kendall, T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: JP 2001520523-A 2 30-OCT-2001;
PIONEER HI BREID INTERNATIONAL INC
PN JP 2001520523-A/2
COMMENT PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAAT, GARY A HUFFMAN,
PI TIMMY L KENDALL
PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC
, C07K14/34, C12Q1/68,
PC A01H5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
SOURCE 1..1394
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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## ORIGIN

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Query Match 100.0%; Score 1311; DB 6; Length 1394;
Best Local Similarity 100.0%; Pred. No. 7,2e-228; Indels 0; Gaps 0;
Matches 1311; Conservative 0; Mismatches 0;

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Qy 1 CCATGAGTCTCTATGAAAAAGATGAGTACATGTCATATCCGTTTCTTAGGGTCC 60
Db 1 CCATGAGTCTCTATGAAAAAGATGAGTACATGTCATATCCGTTTCTTAGGGTCC 60
Qy 61 CTTCTTCTGCTTATATGCTGATGCGGTTTACAAAAAATTCCACGGGTGATGAT 120
Db 61 CTTCTTCTGCTTATATGCTGATGCGGTTTACAAAAAATTCCACGGGTGATGAT 120
Qy 121 CTCATGTTCCATCTTCCACCTCGCGTTGACATTTCTTGAGATGCGGTGTTCCAT 180
Db 121 CTCATGTTCCATCTTCCACCTCGCGTTGACATTTCTTGAGATGCGGTGTTCCAT 180
Qy 181 CTGACCGAGGCCCATCAGACACCTTTGCGGACACCCCATCAAGGGCTTTGCGATGCCA 240
Db 181 CTGACCGAGGCCCATCAGACACCTTTGCGGACACCCCATCAAGGGCTTTGCGATGCCA 240

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QY	241	CGAGAGTATCGGGTGGTGTATCGAGGGGATATATGTGTCCTCCACATGTCACCTATA	300
DB	241	CGAGAGTATCGGGTGGTGTATCGAGGGGATATATGTGTCCTCCACATGTCACCTATA	300
QY	301	TTTATTTCTTTTAAATATTTATTTTGGAAAAATTAACAACCTTAACTTTTGTATA	360
DB	301	TTTATTTCTTTTAAATATTTTGGAAAAATTAACAACCTTAACTTTTGTATA	360
QY	361	GGGCTTCAGCATAGTTTTCCTTGAGGGCCCAAAAATGCGAGACAGGCAATGCTAG	420
DB	361	GGGCTTCAGCATAGTTTTCCTTGAGGGCCCAAAAATGCGAGACAGGCAATGCTAG	420
QY	421	TCACATATTTGGCATCTCCCGAACAAGTTTAAAAATTAACCAAGTAACTTAATCACT	480
DB	421	TCACATATTTGGCATCTCCCGAACAAGTTTAAAAATTAACCAAGTAACTTAATCACT	480
QY	481	CGAAGCTATCATGTATGTTTAAAGAAACATCTATTAACCAAGTAACTTTAAAAAA	540
DB	481	CGAAGCTATCATGTATGTTTAAAGAAACATCTATTAACCAAGTAACTTTAAAAAA	540
QY	541	CAAGCATATTTGAAAAGAGCAAAATATATGTTACAGTTTACAAACATCTAAGAGCAAAA	600
DB	541	CAAGCATATTTGAAAAGAGCAAAATATATGTTACAGTTTACAAACATCTAAGAGCAAAA	600
QY	601	TTATTCGAAGAGTATGATATGACGTGATGATTTTCTTTTCAATCTTGTATTTGTT	660
DB	601	TTATTCGAAGAGTATGATATGACGTGATGATTTTCTTTTCAATCTTGTATTTGTT	660
QY	661	ATTGTTTTATATATTTTCTTCTTAAATAGAGATTTTCTTCCGATTTTATATAA	720
DB	661	ATTGTTTTATATATTTTCTTCTTAAATAGAGATTTTCTTCCGATTTTATATAA	720
QY	721	ATGACTATAAGTATTTTATATATAGAGACGCGATGCTGATGATTTCTGCTCAAAATC	780
DB	721	ATGACTATAAGTATTTTATATATAGAGACGCGATGCTGATGATTTCTGCTCAAAATC	780
QY	781	TTTCTGATTTTAAAGCTATGTCGAAACCTGTTTCTTCAAGAAATTTGATTT	840
DB	781	TTTCTGATTTTAAAGCTATGTCGAAACCTGTTTCTTCAAGAAATTTGATTT	840
QY	841	TTCAAAAAAATTAAGTTATTTCTCTTATATATAATGAAAACATTTGAAAAATAGAGT	900
DB	841	TTCAAAAAAATTAAGTTATTTCTCTTATATATAATGAAAACATTTGAAAAATAGAGT	900
QY	901	TGCGAGCTAGGCTAGAAATGTTTCCCAATTAATTAACATCACTGTATATATATTTG	960
DB	901	TGCGAGCTAGGCTAGAAATGTTTCCCAATTAATTAACATCACTGTATATATATTTG	960
QY	961	GGCGAGCTAGGCTAGAAATGTTTCCCAATTAATTAACATCACTGTATATATATTTG	1020
DB	961	GGCGAGCTAGGCTAGAAATGTTTCCCAATTAATTAACATCACTGTATATATATTTG	1020
QY	1021	TTCTCTAGATTAATTAAG	1080
DB	1021	TTCTCTAGATTAATTAAG	1080
QY	1081	TGAGATGTGCGATTTGGCAAGATGCAACCGTATCATGATGATGATGATGATGATGAT	1140
DB	1081	TGAGATGTGCGATTTGGCAAGATGCAACCGTATCATGATGATGATGATGATGATGAT	1140
QY	1141	GGTTCGAGAGCTCTGTCATCTCATGATGATGATGATGATGATGATGATGATGATG	1200
DB	1141	GGTTCGAGAGCTCTGTCATCTCATGATGATGATGATGATGATGATGATGATGATG	1200
QY	1201	TTGTCATGCTCAAGCTTGGCTATTTGTAACCAAGAGAGATCACTTCCCAACAT	1260
DB	1201	TTGTCATGCTCAAGCTTGGCTATTTGTAACCAAGAGAGATCACTTCCCAACAT	1260
QY	1261	CGATCTATCATGAGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1311
DB	1261	CGATCTATCATGAGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1311

## RESULT 3.

AX224394 1394 bp DNA linear PAT 10-SEP-2001  
 LOCUS AX224394  
 DEFINITION Sequence 1 from Patent WO0160997.  
 ACCESSION AX224394  
 VERSION AX224394.1 GI:15554636  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
 1. Albertsen, M. C., Fox, T. W., Garnaat, C. W., Huffman, G. and Kendall, T. L.  
 Male tissue-derived regulatory region and method of using same  
 Patent: WO 0160997-A 1 23-Aug-2001.  
 JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)  
 FEATURES  
 source  
 1. 1394  
 Location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:4577"

## ORIGIN

Query Match 100.0%; Score 1311; DB 6; Length 1394;  
 Best Local Similarity 100.0%; Pred. No. 7,2e-228;  
 Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	CTTCTTCGCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG	120
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DB	121	CTTCATGCTTCACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180
QY	181	CTGACGAGGCTTCACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	240
DB	181	CTGACGAGGCTTCACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	240
QY	241	CGAGAGCTATGCGGTCGTGATGATGATGATGATGATGATGATGATGATGATGATG	300
DB	241	CGAGAGCTATGCGGTCGTGATGATGATGATGATGATGATGATGATGATGATGATG	300
QY	301	TTATTTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	360
DB	301	TTATTTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	360
QY	361	GGGCTTCAGCATAGTTTTCCTTGAGGGCCCAAAAATGCGAGACAGGCAATGCTAG	420
DB	361	GGGCTTCAGCATAGTTTTCCTTGAGGGCCCAAAAATGCGAGACAGGCAATGCTAG	420
QY	421	TCACATATTTGGCATCTCCCGAACAAGTTTAAAAATTAACCAAGTAACTTAATCACT	480
DB	421	TCACATATTTGGCATCTCCCGAACAAGTTTAAAAATTAACCAAGTAACTTAATCACT	480
QY	481	CGAAGCTATCATGTATGTTTAAAGAAACATCTATTAACCAAGTAACTTTAAAAAA	540
DB	481	CGAAGCTATCATGTATGTTTAAAGAAACATCTATTAACCAAGTAACTTTAAAAAA	540
QY	541	CAAGCATATTTGAAAAGAGCAAAATATATGTTACAGTTTACAAACATCTAAGAGCAAAA	600
DB	541	CAAGCATATTTGAAAAGAGCAAAATATATGTTACAGTTTACAAACATCTAAGAGCAAAA	600
QY	601	TTATTCGAAGAGTATGATATGACGTGATGATTTTCTTTTCAATCTTGTATTTGTT	660
DB	601	TTATTCGAAGAGTATGATATGACGTGATGATTTTCTTTTCAATCTTGTATTTGTT	660
QY	661	ATTGTTTTATATATTTTCTTCTTAAATAGAGATTTTCTTCCGATTTTATATAA	720

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RESULT 4  
LOCUS AX224395 1394 bp DNA linear PAT 10-SEP-2001  
DEFINITION Sequence 2 from Patent WO0160997.  
ACCESSION AX224395  
VERSION AX224395.1 GI:15554637  
KEYWORDS  
SOURCE  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
AUTHORS Alberten, M.C., Fox, T.W., Garnat, C.W., Huffman, G. and Kendall, T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL Patent: WO 0160997-A 2 23-AUG-2001;  
PIONEER HI-BRED INTERNATIONAL, INC. (US)  
FEATURES  
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ORIGIN  
Query Match 100.0%; Score 1311; DB 6; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 7.2e-228;  
Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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|||||  
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Db 61 CTTCCTTGCCCTTATTAAGTAAATCGGGGTTAACAAAACTTCCAGCGGTCATGAT 120  
Qy 121 CTCATGTTCACTTCTCCGACCTCGGTTGACATTTCTTGAATGTCGTTGCCAT 180  
Db 121 CTCATGTTCACTTCTCCGACCTCGGTTGACATTTCTTGAATGTCGTTGCCAT 180  
Qy 181 CTGACCGAGGCCCATGACACCTTTCGGGACCCCATCAAGGGCCTTTCGATGCCCCA 240  
Db 181 CTGACCGAGGCCCATGACACCTTTCGGGACCCCATCAAGGGCCTTTCGATGCCCCA 240  
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Qy 781 TTCTGATTTTATTAAGAGTATTTGGCAACCTGTTCTTCAAGAAATTTGATTTT 840  
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Db 901 TGCCAGACTAGCCCTAGAAATGTTTCCCAATTAATCAATCATGATATATTAATTG 960  
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Db      1081 TGAGATGTCGGTGTGGCAACGATGACACCGTATCATAGTCAAGGCTGATGCA 1140
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Db      1141 GCTTGGCAGCTCTGCTGTGATCTTCATGATGCAATGCTTGTGTAACCGTGTGC 1200
Qy      1201 TTGTTCCATGTCGCAAGCTTGTGCTTATTCGACCAAGAGATGCTTCCCAACAT 1260
Db      1201 TTGTTCCATGTCGCAAGCTTGTGCTTATTCGACCAAGAGATGCTTCCCAACAT 1260
Qy      1261 CCATCTTACTCATGCACTTCATGCAACGACGACATATGTTTCTGTAAC 1311
Db      1261 CCATCTTACTCATGCACTTCATGCAACGACGACATATGTTTCTGTAAC 1311
Qy      1311 CCATCTTACTCATGCACTTCATGCAACGACGACATATGTTTCTGTAAC 1311

RESULT 5
AF360356 3343 bp DNA linear PLN 12-MAY-2001
LOCUS Zea mays male fertility protein (M645) gene, complete cde.
DEFINITION
ACCESSION AF360356
VERSION AF360356.1 GI:14028756
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
AUTHORS Fox,T.W., Trimmell,M.R. and Albertsen,M.C.
TITLE Cloning of M645, a gene required for male fertility from Zea mays
JOURNAL Unpublished
AUTHORS Fox,T.W., Trimmell,M.R. and Albertsen,M.C.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2001) Trait and Technology Development, Pioneer
IA 50131-1004, USA
IA 50131-1004, USA
FEATURES
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1.3343
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TGBLYADAYVGLWVQSGVASSVAREADQPIRFANDLVHRGVSFFPLDSMKY
SRKDHNLILLEGEGRLIAYDPEISGVHVLGLVFPNGVQISEHQLFLSESTNY
RIMRYMLEPRAGEVFAVLPDPDNVRSRGQFWALIDCCCTGADQVFAKPMIR
TLVEKPLSLKVLTKAARMTVIALIDEGHVVLEDRGHEVMKLVSEVRGSK
LWIGTVAHNHIAITIPYLED"
ORIGIN
Query Match 100.0%; Score 1311; DB 15; Length 3343;
Best Local Similarity 100.0%; Pred. No. 6,2e-228;
Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATGCTGCTATGAAAGATGATGATGCTATGCTTATTCGTTTCTTGGCTCC 60
Db 1 CCATGCTGCTATGAAAGATGATGATGCTATGCTTATTCGTTTCTTGGCTCC 60

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Db      1141  GTTTCGAGCTCTGCTGATCTACATGACATCTCACTGTTCAACCGTGGTC
Qy      1201  TTGTTTCATGCTGCAAGCCTTGCTATTCGACCAAGAGATACCTACTCCCAACAT
Db      1201  TTGTTTCATGCTGCAAGCCTTGCTATTCGACCAAGAGATACCTACTCCCAACAT
Qy      1261  CCATCTTACTGATGCAACTTCATGCAACGACGACATATGTTCTGTAAC
Db      1261  CCATCTTACTGATGCAACTTCATGCAACGACGACATATGTTCTGTAAC

RESULT 6
AX224402      255 bp      DNA      linear      PAT 10-SEP-2001
LOCUS      Sequence 9 from Patent WO0160997.
DEFINITION      AX224402
ACCESSION      AX224402
VERSION      AX224402.1 GI:15554644
KEYWORDS
SOURCE
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS      Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE      Male tissue-preferred regulatory region and method of using same
JOURNAL      PATENT: WO 0160997-A 9 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
SOURCE
1..255
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

ORIGIN
Query Match      12.3%; Score 160.6; DB 6; Length 255;
Best Local Similarity 97.6%; Pred. No. 4.5e-19;
Matches 163; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1145  CGCGAGCTCTGCTGATCTGACATGCACTACTACATGCTTGTCAACCGTTCGTTGT
Db      5      CCGGGAGATCCGTCATCTGACATGCAAGGATGCTTGTCAACCGTTCGTTGT
Qy      1205  TCCATGCTGCAAGCCTTGCTATTCGACCAAGAGATACCTACTCCCAACATTCAT
Db      65      TCCATGCTGCAAGCCTTGCTATTCGACCAAGAGATACCTACTCCCAACATTCAT
Qy      1265  CTTACTCATGCAACTTCATGCAACGACGACATATGTTCTGTAAC
Db      125      CTTACTCATGCAACTTCATGCAACGACGACATATGTTCTGTAAC

RESULT 7
AX224396      158 bp      DNA      linear      PAT 10-SEP-2001
LOCUS      Sequence 3 from Patent WO0160997.
DEFINITION      AX224396
ACCESSION      AX224396
VERSION      AX224396.1 GI:15554638
KEYWORDS
SOURCE
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS      Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE      Male tissue-preferred regulatory region and method of using same
JOURNAL      PATENT: WO 0160997-A 3 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
SOURCE
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ORIGIN
Query Match      11.1%; Score 146; DB 6; Length 158;
Best Local Similarity 99.4%; Pred. No. 2.2e-16;
Matches 157; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1155  CGTTCATCTCACATGACATGCACTGCTGTTCAACCGTGGTC-TTGTTTCATGTC
Db      1      CGTTCATCTCACATGACATGCACTGCTGTTCAACCGTGGTTCATGTC
Qy      1214  CAAGCTTGCTCTATTCTGAAACCAAGAGATACCTACTCCCAACATCTTACTCAT
Db      61      CAAGCTTGCTCTATTCTGAAACCAAGAGATACCTACTCCCAACATCTTACTCAT
Qy      1274  GCAACTTCATGCAACGACGACATATGTTCTGTAAC
Db      121      GCAACTTCATGCAACGACGACATATGTTCTGTAAC

RESULT 8
AC155584      188283 bp      DNA      linear      HTG 25-JAN-2005
LOCUS      Zea mays strain B73 clone ZMMBc0196114, *** SEQUENCING IN PROGRESS
DEFINITION      *** 20 unordered pieces.
ACCESSION      AC155584
VERSION      AC155584.2 GI:58082443
KEYWORDS      HTG; HTGS_PHASE1.
SOURCE
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 188283)
Chan,A.P., Perlea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Uterback,T.R., Feldblyum,T.V., Rabnowicz,P., Fraser,C.M.,
Schubert,K., Sam Miguel,P., Ma,J., Pontoroli,A.C., Rohlfing,T.,
Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and
Quackenbush,J.
Consortium for Maize Genomics - BAC skm sequencing and assembly
Unpublished
2 (bases 1 to 188283)
Chan,A.P., Perlea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Uterback,T.R., Feldblyum,T.V., Rabnowicz,P., Fraser,C.M.,
Schubert,K., Sam Miguel,P., Ma,J., Pontoroli,A.C., Rohlfing,T.,
Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and
Quackenbush,J.
Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 188283)
Chan,A.P., Perlea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Uterback,T.R., Feldblyum,T.V., Rabnowicz,P., Fraser,C.M.,
Schubert,K., Sam Miguel,P., Ma,J., Pontoroli,A.C., Rohlfing,T.,
Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and
Quackenbush,J.
Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57863105.
----- Trace submission
Center name: TIGR
Seq_id: ZGFX
----- Project information
Web site: http://www.cigr.org/tcd/cgi/maize/
Contact: maize@cigr.org
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

```



JOURNAL  
 Submitted (19-DEC-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 186199)  
 Biren, B., Nushom, C., Lander, E., Butler, E., Wang, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhvalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardina, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Katat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matchew, C., McCarthy, M., Meldrum, J., Menue, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhphang, P., Pierre, N., Rachupka, A., Ramasamy, V., Raymond, C., Rella, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
 Submitted (17-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Aug 17, 2004 this sequence version replaced gi:49658659.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center  
 Center: Whitehead Institute/MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@road.mit.edu

-----  
 Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
 (http://pgit.rutgers.edu)  
 Butler, E and Wang, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)

-----  
 Project Information  
 Center project name: 130003  
 Center clone name: 334\_A\_1

-----  
 Consensus Information  
 This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository  
 (http://www.ncbi.nlm.nih.gov/traces/trace.cgi). An exact list of reads used in this assembly are available at  
 http://www.broad.mit.edu/annotation/plants/maize/randomclones.html.

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 NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 100617: contig of 100617 bp in length  
 \* 100618 100717: gap of unknown length  
 \* 100718 104730: contig of 4013 bp in length

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 DB 162058 CTTTCGATTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGAATTTGATT 162116  
 QY 840 TTCAAAAATAATGTTATTTCTCTTTATTAATAAGAAACCTAGAAAAATGAG 899  
 DB 162117 TTCTAAGTGAATAGTTCAATTTCTCTTAACAAATGAATTTATGTAATAATGAG 162176  
 QY 900 TTGGCAGACTAGCCCTGAATGTTTCCCAATAATTAACA 940  
 DB 162177 TTTCCAACTACCTCAAGATTAATGAATGACGACAA 162217

RESULT 10  
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 ACCSSION  
 CR936840.2 GI:60302473  
 KEYWORDS  
 HTG; HTGS; PHASE1  
 SOURCE  
 Danio rerio (zebrafish)  
 ORGANISM  
 Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 161616)  
 Smit, S.  
 Direct Submission  
 Submitted (24-FEB-2005) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk clone requests: clonerequests@sanger.ac.uk  
 On Feb 26, 2005 this sequence version replaced gi:60279457.

-----  
 COMMENT  
 Genomes Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
 Project Information  
 Center project name: zK91021  
 Summary Statistics

Assembly program: XGAP4; version 4.5  
 Chemistry: Dye-terminator; 100% of reads  
 Consensus quality: 156361 bases at least Q40  
 Consensus quality: 157330 bases at least Q30  
 Consensus quality: 158179 bases at least Q20  
 Insert size: 160416; sum-of-contigs  
 Insert size: 160313; 4.7% error; aggrorse-fp  
 Quality coverage: 6.55% in Q20 bases; sum-of-contigs Quality  
 coverage: 6.56% in Q20 bases; aggrorse-fp

NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 13 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of 'N', but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 3158: contig of 3158 bp in length  
 \* 3159 3258: gap of 100 bp.  
 \* 3259 11860: contig of 8602 bp in length  
 \* 11861 11960: gap of 100 bp  
 \* 11961 21800: contig of 9840 bp in length  
 \* 21801 21900: gap of 100 bp  
 \* 21901 45034: contig of 23134 bp in length  
 \* 45035 47371: contig of 2237 bp in length  
 \* 47372 47471: gap of 100 bp  
 \* 47471 66272: contig of 19256 bp in length  
 \* 66272 66827: gap of 100 bp  
 \* 66828 79067: contig of 12240 bp in length  
 \* 79068 79167: gap of 100 bp  
 \* 79168 97493: contig of 18226 bp in length  
 \* 97494 103543: gap of 100 bp  
 \* 103543 103642: gap of 100 bp  
 \* 103642 112675: contig of 6049 bp in length  
 \* 112676 112775: gap of 100 bp  
 \* 112776 137298: contig of 24523 bp in length  
 \* 137299 137398: gap of 100 bp  
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 636 TCTTTTCATCTGTTATTTGTTATTTGTTTATATATACATTTCTCTTACATG  
 79251 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT  
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 79311 TTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT  
 756 TGTGTGTGATCTGCTCAAAAATCTTCTGATTTTATTTTATTTTATTTATTTATTT  
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 816 GTTCTTTCAAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT  
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 876 TGAAGAACTTGAAGAAATGAGTTGCGACACTGACCTAGATTTTCCCATTAAT  
 79491 TAAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT  
 936 TACATCATCTGTATTAATTTT 959  
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RESULT 11  
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 AX4  
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 VERSION AC117267.2 GI:42733680  
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 SOURCE Dictyostelium discoideum  
 ORGANISM Dictyostelium discoideum  
 BUKARYOTA; Mycetozoa; Dictyostellida; Dictyostellum.  
 REFERENCE  
 1 (bases 1 to 25769)  
 Gloeckner,G., Eichinger,L., Szafrański,K., Pachatz,J., Dear,P.,  
 Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,  
 Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and  
 Noegel,A.A.  
 Sequence and analysis of chromosome 2 of Dictyostelium discoideum  
 Nature 418 (6893), 79-85 (2002)  
 JOURNAL  
 PUBMED 12097910  
 REMARK The Dictyostelium Genome Sequencing Consortium  
 REFERENCE 2 (bases 1 to 25769)  
 AUTHORS Baumgart,C.  
 TITLE Direct Submission

JOURNAL Submitted (09-APR-2002) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstr. 11, Jena 07745, Germany  
REFERENCE 3 (bases 1 to 25769)  
AUTHORS Baumgart, C.  
JOURNAL Direct Submission  
COMMENT Submitted (21-FEB-2004) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstr. 11, Jena 07745, Germany  
On or before Feb 21, 2004 this sequence version replaced  
gi:19570016, gi:20087114.  
CDS predictions from Genaid may contain errors. Further information  
is available from IMB Jena, Department of Genome Analysis  
(http://genome.imb-jena.de/dictyostelium/) and the University Cologne, Institute for Biochemistry I  
(http://www.uni-koeln.de/dictyostelium/project.shtml)  
Funding Agency : Deutsche Forschungsgemeinschaft (DFG).  
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CKYSNLSLLEGEIIPNKOSVEYVLSPTSTGSGRESIIICYDVGSMGIT  
EYPSLOSFWNAKKGVKGSASGSPYISLFCVOSIIPMIDRLIOYKRWLVTS  
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TDVEMSLICHLPTLEINKYDSKQLSRVKQEPNVSITDLTLVSSRRPFEVQIYP  
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SLGQNW.PROLKHLRGHKROOPTIKMGOLPSSLTSLIDBRSVKGVTEIGSIDSVT  
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* 156639 156738: gap of unknown length
* 156739 167111: contig of 10373 bp in length
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* 168222 168321: gap of unknown length
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FEATURES  
Source Location/Qualifiers

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#### ORIGIN

Query Match 5.5%; Score 72.4; DB 14; Length 172293;  
Best Local Similarity 78.6%; Pred. No. 0.0016;  
Matches 99; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

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Qy 791 TTTTAAAGCTAGTTTGGCAACCTGTTCTTCAAGAATTTGATTTTTCAAAAA 850
Db 27185 TGTTAAGAGCTAGTTTGGCAACCTCGTTT-TTCCAAGAAATTTCTATTTTCCCAAGGAAA 27127
Qy 851 ATTAGTTATTTTCTCTTTATTAATAAACAACCTTGAAGAAATGAGTTGCAGACTA 910
Db 27126 ATTAGTTATTTTCTCTTTATTAATAAACAACCTTGAAGAAATGAGTTGCAGACTA 27067
Qy 911 GCCCTA 916
Db 27066 GCCCTA 27061

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#### RESULT 13

AC155618/c 201985 bp DNA linear HTG 25-JAN-2005  
LOCUS Zea mays strain B73 clone ZM5618B0131C15  
DEFINITION \*\*\* 21 unordered pieces.

ACCESSION AC155618  
VERSION AC155618.2 GI:58082477  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE Zea mays  
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 201985)

#### REFERENCE

Chan, A.P., Perrea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,  
Uteirack, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,  
Schubert, K., Samiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,  
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and  
Quackenbush, J.  
Consortium for Maize Genomics - BAC skim sequencing and assembly

#### TITLE

#### JOURNAL

#### REFERENCE

#### AUTHORS

#### TITLE

Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),  
9712 Medical Center Dr, Rockville, MD 20850

#### REFERENCE

#### AUTHORS

Chan, A.P., Perrea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,  
Uteirack, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,  
Schubert, K., Samiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,  
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and

TITLE  
JOURNAL  
COMMENT

Quackenbush, J.  
Direct Submission  
Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR)  
9712 Medical Center Dr. Rockville, MD 20850  
On Jan 25, 2005 this session version replaced gi:57863139.  
Trace submission  
Center name: TIGR  
Seq\_id: ZGCW

Project information  
Web site: <http://www.tigr.org/tdb/egz/maize/>  
Contact: [maize@tigr.org](mailto:maize@tigr.org)

NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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## ORIGIN

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Best Local Similarity 76.9%; Pred. No. 0.0022; Mismatches 29; Indels 1; Gaps 1;  
Matches 100; Conservative 0

QY 792 TTAAAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTTTCAAAAAA 851  
DB 44986 TTAAAGGCTAGTTGGCAACCTATTT-TTCAAGGATTTTCCAAAGAAAA 44928  
QY 852 TAGTTATTTCTCTTATATAATGAAAACTTGAATAATAGTTGCCAAGTNG 911  
DB 44927 TAGTTCAATTTCCATGAAAAATGAAATCCCATGGAAATGTATGCCAAACTNG 44868  
QY 912 CCTTGAATG 921  
DB 44867 CCTTAAAG 44858

RESULT 14  
AF034389/c 713 bp DNA linear INV 04-FEB-1999  
LOCUS Plasmodium falci-parum sexual stage antigen (s16) gene, promoter and partial cds.  
DEFINITION Plasmodium falci-parum sexual stage antigen (s16) gene, promoter and partial cds.  
ACCESSION AF034389  
VERSION AF034389.1 GI:3098290  
KEYWORDS  
ORGANISM Plasmodium falci-parum (malaria parasite P. falci-parum)  
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
AUTHORS Deckerling, K.J., Kaan, A.M., Mbacham, W., Wirth, D.F., Eling, W., Koning, R.N. and Stunnenberg, H.G.  
TITLE Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria parasite Plasmodium falci-parum  
JOURNAL Mol. Cell. Biol. 19 (2), 967-978 (1999)  
PUBMED 9891033





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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:08:23 ; Search time 872.437 Seconds  
(without alignments)

10014.946 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1\_1311

Sequence: 1 ccattgtgtctctatgaaa.....cgacatatgtttcctgaac 1311

Scoring table: IDENTITY\_NUC

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
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Not exceeding Minimum Match 08

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21: \*

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2:  genseseqn1990s: *
3:  genseseqn2000s: *
4:  genseseqn2001as: *
5:  genseseqn2001bs: *
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7:  genseseqn2002bs: *
8:  genseseqn2003as: *
9:  genseseqn2003bs: *
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12: genseseqn2004as: *
13: genseseqn2004bs: *
14: genseseqn2005bs: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1311	100.0	1394	2	AAK07408	Aak07408 Zsa may
2	1311	100.0	1394	2	AAK07409	Zsa may
3	1311	100.0	1394	5	AAH76332	Z. may M
4	1311	100.0	1394	5	AAH76333	Z. may M
5	160.6	12.3	255	5	AAH76340	Z. may M
6	146	11.1	158	5	AAH76334	Z. may M
7	74	5.6	320	13	ADK48600	Plant full
8	74	5.6	624	13	ADK34444	Plant full
9	72.8	5.6	2445	13	ADK61650	Plant full
10	71.8	5.5	928	13	ADK34996	Plant full
11	71.8	5.5	2537	13	ADK61114	Plant full
12	71.8	5.5	3607	13	ADK60218	Plant full
13	70.2	5.4	883	4	AAI15210	Human Dre
14	70.2	5.4	960	11	ACN85231	Breast ca
15	69.8	5.3	13400	13	ADK04286	Corn F1 H
16	69.2	5.3	527	13	ADK09416	Plant full
17	68.4	5.2	1215	13	ADK49964	Plant full
18	68	5.2	1092	14	AE828609	Maize pol
19	67.8	5.2	928	13	ADK34936	Plant full

1	C	20	67.4	5.1	1260	13	ABX60038	Plant full
2	C	21	67.4	5.1	2232	13	ADX3787	Plant full
3	C	22	67.2	5.1	2249	13	ADX45524	Plant full
4	C	23	67.2	5.1	2657	2	AA10551	DNA sequ
5	C	24	66.4	5.1	6627	2	AA58751	Maize full
6	C	25	66.4	5.1	6027	2	ABK09935	DNA encod
7	C	26	66.4	5.1	6027	12	ABK12106	Plant full
8	C	27	66.2	5.0	4339	8	ABK35844	Bovine ES
9	C	28	66	5.0	1376	13	ABO83353	Plant full
10	C	29	65.6	5.0	346	4	AB187279	Human pol
11	C	30	65.6	5.0	2274	13	ABO82310	Plant full
12	C	31	65.6	5.0	2274	13	ABO82057	Plant full
13	C	32	65.6	4.9	8056	8	ABX89714	Human ES
14	C	33	64.6	4.9	9859	13	ABX89440	Oligonuci
15	C	34	64.4	4.9	9859	13	ABX89440	Oligonuci
16	C	35	64	4.9	8056	8	ABX210100	Hematozo
17	C	36	63.8	4.9	431	8	ABX44556	Bovine ES
18	C	37	63.6	4.9	335913	5	AA161371	Soybean 2
19	C	38	63.6	4.9	335913	5	AA161372	Soybean 2
20	C	39	63.4	4.8	12968	4	AA84594	Chemicali
21	C	40	63.4	4.8	12968	4	AA846779	Yemour su
22	C	41	63.4	4.8	12968	4	AB134085	Human imm
23	C	42	63.4	4.8	12968	6	ABX84824	DNA trans
24	C	43	63.4	4.8	12968	6	ABN80285	Human che
25	C	44	63.2	4.8	1340	14	AD271035	Human ch
26	C	45	63	4.8	7624	6	AB134113	Human imm

## ALIGNMENTS

RESULT 1  
AA07408  
TD AA07408 standard. DNA: 1394 BP.

DT 08-JUN-1999 (first entry)

Zea mays Ms45 male tissue-preferred regulatory region

KW Ms45; male; tissue-preferred; regulatory region; plant cells; KW plant tissue; differentiated; maize; hybrid seed; fertility; ss

OS . Zea mays .

PN W09859061-A1

PD 30-DEC-1998.  
VY

PF 19-JUN-1998; 98WO-US012895.  
XX

PR 23-JUN-1997; 9/US-00880499.  
XX

PA (PION-) PIONEER HI-BRED INT. INC.  
XX

AA WPI; 1999-105628/09  
DR

**PT** New nucleic acid encoding a Ms45 male tissue-preferred regulatory region useful for mediating plant fertility associated seed production

XX  
PS Claim 2, Page 22-23: 39pp: English.

The sequence is that encoding an *ans1a5* male tissue-preferred regulatory CC region. It may be used in the construction of a vector for a method of CC producing exogenous genes in a male tissue-preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monoco/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably *Ms45*), which encodes a product selected from auxins, rols and gibberella toxin. Hybrid seeds are produced by cross-pollinating maize male fertile



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OY 1 CCATGGTGTCTCTATGAAAAAGTAGTACATGTCATATGCTTTTCTTAGGGTCC 60
DB 1 CAGAGGTCTCTATGAAAAAGTAGTACATGTCATATGCTTTTCTTAGGGTCC 60
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OY 181 CTGACGAGGCCCCATCAGACACCTTTCGGGACACCCATCAAGGGCTTTTCGATGGCCCA 240
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DB 1261 CCATCTTACTGATGCACTTTCATGCAACAGCAAGCATATGTTCCGTGAC 1311

RESULT 3
AAH76332
ID AAH76332 standard; DNA; 1394 BP.
XX
XX AC AAH76332;
XX
XX 23-OCT-2001 (first entry)
XX
XX DE Z. mays M45 male tissue-preferred regulatory region encoding DNA.
XX
XX KM M45; male tissue; regulatory region; transcription; male fertility;
XX hybrid seed; ds.
XX
XX OS Zea mays.
XX
XX PN W0200160997-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 13-FEB-2001; 2001MO-US004527.
XX
XX PR 15-FEB-2000; 2000US-00504487.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX
XX DR WPI; 2001-514772/56.
XX
XX PS Claim 4; Page 46; 50pp; English.
XX
XX CC The invention provides a male tissue-preferred regulatory region (1)
XX comprising nucleotide sequences essential for initiating transcription of
XX the M45 gene. A method of mediating male fertility in a plant is
XX provided that involves introducing an expression vector comprising a
XX promoter operably linked to (1) into a plant where the exogenous gene
XX impacts male fertility of the plant and (1) controls expression of the
XX present sequence represents a nucleic acid sequence encoding an M45 male
XX tissue preferred regulatory region from Z. mays
XX
XX SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;

Query Match 100.0%; Score 1311; DB 5; Length 1394;
Best Local Similarity 100.0%; Pred. No. 1,2e-265; Indels 0; Gaps 0;
Matches 1311; Conservative 0; Mismatches 0;

OY 1 CCATGGTGTCTCTATGAAAAAGTAGTACATGTCATATGCTTTTCTTAGGGTCC 60
DB 1 CCATGGTGTCTCTATGAAAAAGTAGTACATGTCATATGCTTTTCTTAGGGTCC 60
OY 61 CTCTCTGCTTATATCTGATGATGGGGTTACAAAACTTCCAGGGGTGATGAT 120
DB 61 CTCTCTGCTTATATCTGATGATGGGGTTACAAAACTTCCAGGGGTGATGAT 120

```

Dp	61	CTTCTTCTGCTTATTTACTGACTGAATCGGGGTTTACAAAACCTTCCACGGGTGCATGAT	120
Qy	121	CTCCATGTTCCACCTTCTCCACCTCGGGTGGCACATTTCTTGGATGTCGGTGGTTCCCAT	180
Dp	121	CTCCATGTTCCACCTTCTCCACCTCGGGTGGCACATTTCTTGGATGTCGGTGGTTCCCAT	180
Qy	181	CTGACCCGAGGCCCATCAGACACCTTTGGGGACACCCATCAAGGGCTTTGGGATGGGCCA	240
Dp	181	CTGACCCGAGGCCCATCAGACACCTTTGGGGACACCCATCAAGGGCTTTGGGATGGGCCA	240
Qy	241	CGAAGACGATCGGGTCGTGGTATCCAGGGGATATATGTCCGCCCAATCGTCACTATA	300
Dp	241	CGAAGACGATCGGGTCGTGGTATCCAGGGGATATATGTCCGCCCAATCGTCACTATA	300
Qy	301	TTATTTATTTCTTTAGATATTTATTTAATTTTGGAAAAATTAACAACTTATACCTTTGTGA	360
Dp	301	TTATTTATTTCTTTAGATATTTATTTAATTTTGGAAAAATTAACAACTTATACCTTTGTGA	360
Qy	361	GGGGCTCAGCATTAATTTTGGCTTAAAGGCCCCAGAAATGCGAGGACCAAGCCATGCTAGTG	420
Dp	361	GGGGCTCAGCATTAATTTTGGCTTAAAGGCCCCAGAAATGCGAGGACCAAGCCATGCTAGTG	420
Qy	421	TCGACTATGSGACATACCCAGAACAAAGTTTAAAAAAAATAACAAAGTAACTATCCACT	480
Dp	421	TCGACTATGSGACATACCCAGAACAAAGTTTAAAAAAAATAACAAAGTAACTATCCACT	480
Qy	481	CGAAAGCTATCATGTAAATGTTTAAAGAAACATCTATTAAACCAACGATCCTCTTAAAAAA	540
Dp	481	CGAAAGCTATCATGTAAATGTTTAAAGAAACATCTATTAAACCAACGATCCTCTTAAAAAA	540
Qy	541	CAAGCATTTTCGAAAGAGACAAATATGTTTACAGTTTACAAACATCTAAGAGGACAA	600
Dp	541	CAAGCATTTTCGAAAGAGACAAATATGTTTACAGTTTACAAACATCTAAGAGGACAA	600
Qy	601	TTATATCGAAAGGTAAAGCTATGAGGTTTTCATTTCTTTCAATCTGTATATTTGTT	660
Dp	601	TTATATCGAAAGGTAAAGCTATGAGGTTTTCATTTCTTTCAATCTGTATATTTGTT	660
Qy	661	ATTGTTTTTATATACATTTTCTTCTCTTACATAGAGTATTTTCTTCGATTTTATPAA	720
Dp	661	ATTGTTTTTATATACATTTTCTTCTCTTACATAGAGTATTTTCTTCGATTTTATPAA	720
Qy	721	ATGACTATAAAGTCATTTTATATPAGAGCACGCAATGTCGTAGATCTCGTTCAAAATC	780
Dp	721	ATGACTATAAAGTCATTTTATATPAGAGCACGCAATGTCGTAGATCTCGTTCAAAATC	780
Qy	781	TTTCGATTTTTTTTAAAGCTAGTGTGGCAACCCGTTCCTTCAAAAGATTTTGATTTT	840
Dp	781	TTTCGATTTTTTTTAAAGCTAGTGTGGCAACCCGTTCCTTCAAAAGATTTTGATTTT	840
Qy	841	TTCAAAAAAAATAGTTTATTTTCTCTTATPAAATAGAAAACACTTAGAAAAATAGAGT	900
Dp	841	TTCAAAAAAAATAGTTTATTTTCTCTTATPAAATAGAAAACACTTAGAAAAATAGAGT	900
Qy	901	TGCCAGACTAGCCCTAGATGTTTTCCCAATPAAATTAACAATCACTGTGTATTAATTATG	960
Dp	901	TGCCAGACTAGCCCTAGATGTTTTCCCAATPAAATTAACAATCACTGTGTATTAATTATG	960
Qy	961	GCCAGCCCCCATPAAATTAATTTAAACCGAAATCGAAATCGAGGAAACCAATCTAGCAT	1020
Dp	961	GCCAGCCCCCATPAAATTAATTTAAACCGAAATCGAAATCGAGGAAACCAATCTAGCAT	1020
Qy	1021	TTCTCTAGATTAGTAAAAAGGAGAGAGAGAAAGAAATCAGTTTAACTATGTTGCC	1080
Dp	1021	TTCTCTAGATTAGTAAAAAGGAGAGAGAGAAAGAAATCAGTTTAACTATGTTGCC	1080
Qy	1081	TGAGATGTGCGGTTTGGACAGATAGCCAGCTATATCAATGCTCTAGTGTCTATCGTCA	1140
Dp	1081	TGAGATGTGCGGTTTGGACAGATAGCCAGCTATATCAATGCTCTAGTGTCTATCGTCA	1140
Qy	1141	GTTTGGCAGCTCTGTGTCATCTCAATGGCATCTAATGCTTGTTCACACGTTGCTC	1200
Dp	1141	GTTTGGCAGCTCTGTGTCATCTCAATGGCATCTAATGCTTGTTCACACGTTGCTC	1200

Db	1141	GGTTGCGGACGCTCTCGGNGTCATCTGCACATGAGCATATGACTGCTGTTCAACGGTTCGTC	1200
Qy	1201	TTGTTTCATCATGTCGCAAGCCTTGGCTATTCTTGAAACCAAGAGGATATACCTATCCCAAAACAAAT	1260
Db	1201	TTGTTTCATCATGTCGCAAGCCTTGGCTATTCTTGAAACCAAGAGGATATACCTATCCCAAAACAAAT	1260
Qy	1261	CCATCTTACTCATGCAACATTCGATGCAAAACGACGACATATGTTTCCGTAAC	1311
Db	1261	CCATCTTACTCATGCAACATTCGATGCAAAACGACGACATATGTTTCCGTAAC	1311
RESULT 4			
ID	AAH76333	standard; DNA; 1394 BP.	
AC	AAH76333;		
XX	AAH76333;		
XX	29-OCT-2001	(first entry)	
XX	Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.		
XX	Ms45; male tissue; regulatory region; transcription; male fertility;		
XX	hybrid seed; ds.		
XX	Zea mays.		
XX	W0200160997-h2.		
XX	23-AUG-2001.		
XX	13-FEB-2001; 2001WO-US004527.		
XX	15-FEB-2000; 2000US-00504487.		
XX	(PION-) PIONEER HI-BRED INT INC.		
XX	Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;		
XX	WPI; 2001-514772/56.		
XX	A male tissue-preferred regulatory region comprising nucleotide sequences		
XX	essential for initiating transcription of the Ms45 gene useful for		
XX	mediating fertility in a male plant.		
XX	Claim 4; Page 47; 50pp; English.		
XX	The invention provides a male tissue-preferred regulatory region (I)		
XX	comprising nucleotide sequences essential for initiating transcription of		
XX	the Ms45 gene. A method of mediating male fertility in a plant is		
XX	provided that involves introducing an expression vector comprising a		
XX	promoter operably linked to (I) into a plant where the exogenous gene		
XX	impacts male fertility of the plant and (I) controls expression of the		
XX	exogenous gene. A method of producing hybrid seeds is also provided. The		
XX	present sequence represents a nucleic acid sequence encoding an Ms45 male		
XX	tissue preferred regulatory region from Z. mays		
XX	Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;		
XX	Query Match	100.0%; Score 1311; DB 5; Length 1394;	
XX	Best Local Similarity	100.0%; Pred. No. 1,2e-269;	
XX	Matches 1311; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	CCATGAGTGTCTCTATGAAAAAGATGAGTACATGTGCTATATCCGTTTCTTAAAGGTC	60
Db	1	CCATGAGTGTCTCTATGAAAAAGATGAGTACATGTGCTATATCCGTTTCTTAAAGGTC	60
Qy	61	CTTCTTTCGCTTATTAATGACTGTAATCGGGGTTTACAAAAAATTCCACGGGTGCATGAT	120
Db	61	CTTCTTTCGCTTATTAATGACTGTAATCGGGGTTTACAAAAAATTCCACGGGTGCATGAT	120
Qy	121	CTTCATGTTCCACTTCCCACTCCGAGTTCGACATTTCTTGAGATGCGGTGTTCCCAT	180
Db	121	CTTCATGTTCCACTTCCCACTCCGAGTTCGACATTTCTTGAGATGCGGTGTTCCCAT	180

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OY 181 CTGACGAGGCGCCATGACGACCTTTGGGGAACCCATGAAGGCGCTTTGGAGGCCCA 240
DB 181 CTGACGAGGCGCCATGACGACCTTTGGGGAACCCATGAAGGCGCTTTGGAGGCCCA 240
OY 241 CGAGAGCTATCGGCTGCTGTGATCCAGGGGATATATGCTCCCAATTCGACATATA 300
DB 241 CGAGAGCTATCGGCTGCTGTGATCCAGGGGATATATGCTCCCAATTCGACATATA 300
OY 301 TTTATATCTTGAATATATATTTTATTTTGAATAAATAAATAAATAAATAAATAAATA 360
DB 301 TTTATATCTTGAATATATATTTTATTTTGAATAAATAAATAAATAAATAAATAAATA 360
OY 361 GGGGCTCAGATATGATTTTGGCTTGAAGGCGCGAATAATGCGAGGACCAAGCATGCTAGT 420
DB 361 GGGGCTCAGATATGATTTTGGCTTGAAGGCGCGAATAATGCGAGGACCAAGCATGCTAGT 420
OY 421 TCCACTATGGGCTACCGCAAGAACAGATTTTAAATAAATAAATAAATAAATAAATAAATA 480
DB 421 TCCACTATGGGCTACCGCAAGAACAGATTTTAAATAAATAAATAAATAAATAAATAAATA 480
OY 481 CGAAGCTATCATATGATATGATTTTAAAGAAATCATTTTAAACAGATCCTCTTAAATAA 540
DB 481 CGAAGCTATCATATGATATGATTTTAAAGAAATCATTTTAAACAGATCCTCTTAAATAA 540
OY 541 CAGAGATATTTGAAAGAGACAAATATGATTCAGTTTCAAAATCTTAAGAGGACGAA 600
DB 541 CAGAGATATTTGAAAGAGACAAATATGATTCAGTTTCAAAATCTTAAGAGGACGAA 600
OY 601 TTTATATCGAAGAGTATGATGAGTTCAGTTCATTTCTTTCTTTCTTTCTTTCTTTCTT 660
DB 601 TTTATATCGAAGAGTATGATGAGTTCAGTTCATTTCTTTCTTTCTTTCTTTCTTTCTT 660
OY 661 ATTTGTTTTTATATACATTTCTTCTTCAATATGATGATTTTCTTCCGATTTTATATA 720
DB 661 ATTTGTTTTTATATACATTTCTTCTTCAATATGATGATTTTCTTCCGATTTTATATA 720
OY 721 ATGACTATTAAGTATTTTATATTAATTAAGACAGGATGCTGATTCCTGCTTCAAAATC 780
DB 721 ATGACTATTAAGTATTTTATATTAATTAAGACAGGATGCTGATTCCTGCTTCAAAATC 780
OY 781 TTTCTGATTTTAAAGCTATGATGAGACCCGTTTCTTCAAGATTTTGAATTTT 840
DB 781 TTTCTGATTTTAAAGCTATGATGAGACCCGTTTCTTCAAGATTTTGAATTTT 840
OY 841 TTTCAAAAAAATTAATTTTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 900
DB 841 TTTCAAAAAAATTAATTTTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 900
OY 901 TCCAGACTAGCCCTAGATGTTTCCCAATTAATTAATTAATTAATTAATTTT 960
DB 901 TCCAGACTAGCCCTAGATGTTTCCCAATTAATTAATTAATTAATTAATTTT 960
OY 961 GCGAGCCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 961 GCGAGCCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
OY 1021 TTTCTGATTTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 TTTCTGATTTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
OY 1081 TGAATTTGCTGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 TGAATTTGCTGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
OY 1141 GGTTCGAGAGCTCTGCTGATCTGACATGAGATCTATGCTTTTCAACGTTTCTGTC 1200
DB 1141 GGTTCGAGAGCTCTGCTGATCTGACATGAGATCTATGCTTTTCAACGTTTCTGTC 1200
OY 1201 TTTGTTCAATCTGTCAGAGCTTGGCTATTTGAAACAGAGAGATTCCTTCCAAACAT 1260
DB 1201 TTTGTTCAATCTGTCAGAGCTTGGCTATTTGAAACAGAGAGATTCCTTCCAAACAT 1260

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OY 1261 CCATCTTACTATGACCACTTCCATGCAACGACACATATGTTCTGTGAC 1311
DB 1261 CCATCTTACTATGACCACTTCCATGCAACGACACATATGTTCTGTGAC 1311

RESULT 5
ID AAH76340 standard; DNA; 255 BP.
AC AAH76340;
XX 29-OCT-2001 (first entry)
DB Z. mays Me45 promoter fragment.
XX Me45; male tissue; regulatory region; transcription; male fertility;
XX hybrid seed; promoter; ds.
OS Zea mays.
PN W0200160997-A2.
XX 23-AUG-2001.
XX 13-FEB-2001; 2001WO-US004527.
XX 15-FEB-2000; 2000US-00504487.
XX (PION-) PIONEER HI-BRED INT INC.
XX Albertsen MC, Fox TW, Garnat CW, Huffman G, Kendall TL;
XX WPI; 2001-514772/56.
XX A male tissue-preferred regulatory region comprising nucleotide sequences
XX essential for initiating transcription of the Me45 gene useful for
XX mediating fertility in a male plant.
XX Example 5; Fig 8; 50bp; English.
XX The invention provides a male tissue-preferred regulatory region (1)
XX comprising nucleotide sequences essential for initiating transcription of
XX the Me45 gene. A method of mediating male fertility in a plant is
XX provided that involves introducing an expression vector comprising a
XX promoter operably linked to (1) into a plant where the exogenous gene
XX impacts male fertility of the plant and (1) controls expression of the
XX exogenous gene. A method of producing hybrid seeds is also provided. The
XX present sequence represents a Z. mays Me45 promoter fragment
XX
XX Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other:
XX
XX Query Match 12.3%; Score 160.6; DB 5; Length 255;
XX Best Local Similarity 97.6%; Pred. No. 1.5e-24;
XX Matches 163; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1145 CCGCAGCTCTGCTGATCTGACATGAGATCTATGATGCTTTGAAACGTTGCTTGT 1204
DB 5 CCGCAGATCCCGTGCATCTGACATGAGATCTATGATGCTTTGAAACGTTGCTTGT 64
OY 1205 TCCATCTGCAAGCCTTGCCTATTTGAAACCAAGAGATACCTACTCCCAACATTCAT 1264
DB 65 TCCATCTGCAAGCCTTGCCTATTTGAAACCAAGAGATACCTACTCCCAACATTCAT 124
OY 1265 CTTACTGATCACTTCCATGCAACGACACATATGTTTCTGTGAC 1311
DB 125 CTTACTGATCACTTCCATGCAACGACACATATGTTTCTGTGAC 171

RESULT 6
ID AAH76334 standard; DNA; 158 BP.
XX AAH76334;
AC AAH76334;

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XX 29-OCT-2001 (first entry)  
XX  
DE Z. may5 Ms45 male tissue-preferred regulatory region fragment.  
XX  
KM Me45; male tissue; regulatory region; transcription; male fertility;  
KM hybrid seed; ds.  
XX  
OS Zea mays.  
XX  
PN WO200160997-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 13-FEB-2001; 2001WO-US004527.  
XX  
PR 15-FEB-2000; 2000US-00504487.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;  
XX WPI; 2001-514772/56.  
DR  
XX A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the MS45 gene useful for  
PT mediating fertility in a male plant.  
XX  
PS Claim 5; Page 47; 50pp; English.  
XX  
CC The invention provides a male tissue-preferred regulatory region (1)  
CC comprising nucleotide sequences essential for initiating transcription of  
CC the MS45 gene. A method of mediating male fertility in a plant is  
CC provided that involves introducing an expression vector comprising a  
CC promoter operably linked to (1) into a plant where the exogenous gene  
CC impacts male fertility of the plant and (1) controls expression of the  
CC exogenous gene. A method of producing hybrid seeds is also provided. The  
CC present sequence represents a DNA fragment -38 to -195 bases upstream of  
CC the RTA box of a Z. mays Ms45 male-tissue preferred regulatory region  
CC nucleotide sequence  
XX  
SQ Sequence 158 BP; 41 A; 50 C; 21 G; 46 T; 0 U; 0 Other;  
Query Match 11.1%; Score 146; DB 5; Length 158;  
Best Local Similarity 99.4%; Pred. No. 1.7e-21;  
Matches 157; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1155 CGTGTCACTTCACATGCAATGCTGTTTCACCGCTTCGTC-TTGTTCATCGTC 1213  
DB 1 CGTGTCACTTCACATGCAATGCTGTTTCACCGCTTCGTTGTTCATCGTC 60  
QY 1214 CAAGCTTGCTTCTGAACCAAGAGATGCTTCCCAAGCAATCATCTTACTGAT 1273  
DB 61 CAAGCTTGCTTCTGAACCAAGAGATGCTTCCCAAGCAATCATCTTACTGAT 120  
QY 1274 GCAACTTCCATGCAAAACGACGACATATGTTTCTGTAAC 1311  
DB 121 GCAACTTCCATGCAAAACGACGACATATGTTTCTGTAAC 158  
RESULT 7  
AD48600 ID ADX48600 standard; cDNA; 320 BP.  
XX  
AC ADX48600;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 23340.  
XX  
KM plant protectant; plant growth regulant; gene therapy; plant;  
KM recombinant DNA construct; physical array; plant breeding marker;  
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KM extreme osmotic condition; pathogen tolerance; pest tolerance;  
KM growth rate; cell cycle pathway; disease resistance;  
KM galactomannan production; lignin production; plant growth regulator;  
KM yield; plant growth; plant development; seed oil; protein yield;  
KM protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/) TABASKA J E.  
PA (CAO/) CAO Y.  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
DR  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 23340; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspso.gov/sequence.html?docid:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 320 BP; 89 A; 53 C; 66 G; 112 T; 0 U; 0 Other;  
Query Match 5.6%; Score 74; DB 13; Length 320;  
Best Local Similarity 73.1%; Pred. No. 4.6e-06;  
Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
QY 791 TTTTAAGAGCTAGTTGGCAACCTGTTCTTTTCAAGAAATTTGATTTTTCAAAAA 850  
DB 62 TTTTAAGAGCTAGTTGGCAATTCATTTTTCACAGAGATTTTATTTTCTTAAAGAA 121  
QY 851 ATTAGTTATTTTCTTTTAAATAAGAAACCTAGAGAAAATAGTGGCAGACTA 910  
DB 122 ATTAGTTATTTTCTTTTGAAGAAATAGAAATCCCTTGGGAAATAGAGTTTCAAGCA 181  
QY 911 GCCCTAGAAAT 920  
DB 182 GCCCTAATT 191

RESULT 8  
ADXX3444  
ID ADXX3444 standard; cDNA, 624 BP.  
XX  
XX ADXX3444;  
XX  
XX 21-APR-2005 (first entry)  
XX  
XX Plant full length insert polynucleotide seqid 16264.  
XX  
XX plant protectant; plant growth regulant; gene therapy; plant;  
XX recombinant DNA construct; physical array; plant breeding marker;  
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
XX extreme osmotic condition; pathogen tolerance; pest tolerance;  
XX growth rate; cell cycle pathway; disease resistance;  
XX galactomanan production; lignin production; plant growth regulator;  
XX yield; plant growth; plant development; seed oil; protein yield;  
XX protein content; gene; ss.  
XX  
XX Unidentified.  
XX  
XX US2004034888-A1.  
XX  
XX 19-FEB-2004.  
XX  
XX 28-APR-2003; 2003US-00425114.  
XX  
XX 06-MAY-1999; 99US-00304517.  
XX PR 05-NOV-2001; 2001US-00985678.  
XX  
XX (LITU/) LIU J.  
XX (ZHOU/) ZHOU Y.  
XX (KOVA/) KOVALIC D K.  
XX (SCRE/) SCREEN S E.  
XX (TABAS/) TABASKA J E.  
XX (CAOV/) CAO Y.  
XX  
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
XX pests, for conferring increased resistance to plant disease, or for  
XX improving yield.  
XX  
XX Claim 1; SEQ ID NO 16264; 15bp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
XX polynucleotide consisting of a sequence encoding an amino acid sequence  
XX available in electronic form from the US patent office at  
XX ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
XX of the invention are also useful in physical arrays of molecules and as  
XX plant breeding markers. The recombinant DNA construct is useful for  
XX improving plant tolerance to cold, heat, drought, herbicides, extreme  
XX osmotic conditions, pathogens or pests, for manipulating growth rate in  
XX plant cells by modification of the cell cycle pathway, for conferring  
XX increased resistance to plant disease, for producing galactomanan,  
XX lignin or plant growth regulators, for increasing the rate of homologous  
XX recombination in plants, for improving yield by modification of  
XX photocynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
XX or by providing improved plant growth and development under at least one  
XX stress condition or for modifying seed oil or protein yield and/or  
XX content. This sequence represents a plant full length insert  
XX polynucleotide that can be used in the recombinant DNA construct of the  
XX invention.  
XX  
XX Sequence 624 BP; 170 A; 119 C; 146 G; 189 T; 0 U; 0 Other;  
XX  
XX Query Match 5.6%; Score 74; DB 13; Length 624;  
XX Best Local Similarity 73.1%; Pred. NO. 5.4e-06;  
XX Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 791 TTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGATTGTTTCAAAAAA 850  
DB 374 TTTTGGCGTAGTTTGGAATCTATTTTTCAGAGATTTTTCTTAAGAA 433  
QY 851 ATTGTTATTTTCTTCTTATTAATAGAAAAACATTAGAAAAATAGTCCGACTA 910  
DB 434 ATTGTTATTTTCTTCTTATTAATAGAAAAATCCCTGGGAAATTAGATTCTTAACGA 493  
QY 911 GCCCTAGAAAT 920  
DB 494 GCCCTTAATT 503  
RESULT 9  
ADXX61650  
ID ADXX61650 standard; cDNA, 2445 BP.  
XX  
XX ADXX61650;  
XX  
XX 21-APR-2005 (first entry)  
XX  
XX Plant full length insert polynucleotide seqid 32493.  
XX  
XX plant protectant; plant growth regulant; gene therapy; plant;  
XX recombinant DNA construct; physical array; plant breeding marker;  
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
XX extreme osmotic condition; pathogen tolerance; pest tolerance;  
XX growth rate; cell cycle pathway; disease resistance;  
XX galactomanan production; lignin production; plant growth regulator;  
XX yield; plant growth; plant development; seed oil; protein yield;  
XX protein content; gene; ss.  
XX  
XX Unidentified.  
XX  
XX US2004034888-A1.  
XX  
XX 19-FEB-2004.  
XX  
XX 28-APR-2003; 2003US-00425114.  
XX  
XX 06-MAY-1999; 99US-00304517.  
XX PR 05-NOV-2001; 2001US-00985678.  
XX  
XX (LITU/) LIU J.  
XX (ZHOU/) ZHOU Y.  
XX (KOVA/) KOVALIC D K.  
XX (SCRE/) SCREEN S E.  
XX (TABAS/) TABASKA J E.  
XX (CAOV/) CAO Y.  
XX  
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
XX pests, for conferring increased resistance to plant disease, or for  
XX improving yield.  
XX  
XX Claim 1; SEQ ID NO 32493; 15bp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
XX polynucleotide consisting of a sequence encoding an amino acid sequence  
XX available in electronic form from the US patent office at  
XX ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
XX of the invention are also useful in physical arrays of molecules and as  
XX plant breeding markers. The recombinant DNA construct is useful for  
XX improving plant tolerance to cold, heat, drought, herbicides, extreme  
XX osmotic conditions, pathogens or pests, for manipulating growth rate in  
XX plant cells by modification of the cell cycle pathway, for conferring  
XX increased resistance to plant disease, for producing galactomanan,  
XX lignin or plant growth regulators, for increasing the rate of homologous  
XX recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 2445 BP; 666 A; 470 C; 513 G; 796 T; 0 U; 0 Other;  
Query Match 5.6%; Score 72.8; DB 13; Length 2445;  
Best Local Similarity 73.6%; Pred. No. 1.4e-05;  
Matches 106; Conservative 0; Mismatches 37; Indels 1; Gaps 1;  
Qy 792 TTTAAGAGCTAGTTGGCAACCTGTTCTT-TCAAGCAATTTGATTTTCAAAAAA 850  
Db 1623 TCTTAGGGCTAGTTGAGAACCTTTTTCCTCCAAAAGATTTTCATTTCAGAAAGAAA 1682  
Qy 851 ATTAGTTATTTTCTCTTTAATAAATAGAAAACACTTGAAGTTGCCAGACTA 910  
Db 1683 ATTAGTTATTTTCTCTTTAATAAATAGAAAATCCTTAAAAAATAGTGTTCAAACTA 1742  
Qy 911 GCCCTAGAAATGTTTCCCAATAA 934  
Db 1743 GCCCTAATGTTTTCATGAA 1766  
RESULT 10  
ADX34996/C  
ID ADX34996 standard; cDNA, 928 BP.  
XX  
AC ADX34996;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 17816.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PP 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LITU/) LITU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
DR WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 17816; 15pp; English.

XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 928 BP; 245 A; 209 C; 219 G; 255 T; 0 U; 0 Other;  
Query Match 5.5%; Score 71.8; DB 13; Length 928;  
Best Local Similarity 78.0%; Pred. No. 1.8e-05;  
Matches 99; Conservative 0; Mismatches 27; Indels 1; Gaps 1;  
Qy 790 TTTTAAAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTTCAAAAAA 849  
Db 804 TTTTAAAGAGCTAGTTGGCA-CCTCATTTTCTAAGGATTTCTATTACTAAGAAA 746  
Qy 850 AATTAGTTATTTTCTCTTTAATAAATAGAAAACACTTGAAGTTGCCAGACT 909  
Db 745 AATTAGTTAATTTTCTCTTGAAGAAAATGAATGAATGCTTGAAGAAATAGAGTTACCAATT 686  
Qy 910 AGCCCTA 916  
Db 685 ACCCTTA 679  
RESULT 11  
ADX61114  
ID ADX61114 standard; cDNA; 2537 BP.  
XX  
AC ADX61114;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 31957.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PP 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LITU/) LITU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.

PA (TABASKA) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX LUU J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX WPI; 2004-180133/17.  
 DR New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX  
 XX Claim 1, SEQ ID NO 31957; 15pp; English.  
 PS  
 XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.  
 CC  
 XX Sequence 2537 BP; 685 A; 484 C; 524 G; 844 T; 0 U; 0 Other;  
 SQ  
 Query Match 5.5%; Score 71.8; DB 13; Length 2537;  
 Best Local Similarity 73.4%; Pred. No. 2.2e-05;  
 Matches 105; Conservative 0; Mismatches 37; Indels 1; Gaps 1;  
 QY 792 TTAAAGGCTAGTGGCAACCGTCTTTCAGAAATTTGATTTTCAAAAAA 851  
 Db TCTTAAGGCTAGTGGCAACCGTCTTTCAGAAATTTGATTTTCAAAAAA 1857  
 QY 852 TTAGTTATTTCTCTTATTAATAATGAAAAACCTTAGAAAAATGAGTGCAGACTAG 911  
 Db TTAGTTATTTCTCTTATTAATAATGAAAAACCTTAGAAAAATGAGTGCAGACTAG 1917  
 QY 912 CCTTAGAATGTTTTCCCAATPAA 934  
 Db CCTTAGAATGTTTTCCCAATPAA 1940  
 RESULT 12  
 ADX60218  
 ID ADX60218 standard; cDNA; 3607 BP.  
 XX  
 XX ADX60218;  
 AC  
 XX 21-APR-2005 (first entry)  
 DT  
 XX  
 XX Plant full length insert polynucleotide seqid 31061.  
 DE  
 XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomanan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content; gene; ss.  
 XX  
 XX Unidentified.  
 XX

PN US200403488-A1.  
 XX 19-FEB-2004.  
 PD  
 XX 28-APR-2003; 2003US-00425114.  
 XX  
 XX 06-MAY-1999; 99US-00304517.  
 PR  
 XX 05-NOV-2001; 2001US-00985678.  
 XX  
 XX (LIU/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCREEN/) SCREEN S E.  
 PA (TABASKA/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX  
 XX LUU J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX WPI; 2004-180133/17.  
 DR New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX  
 XX Claim 1, SEQ ID NO 31061; 15pp; English.  
 PS  
 XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.  
 CC  
 XX Sequence 3607 BP; 915 A; 695 C; 718 G; 1279 T; 0 U; 0 Other;  
 SQ  
 Query Match 5.5%; Score 71.8; DB 13; Length 3607;  
 Best Local Similarity 73.4%; Pred. No. 2.4e-05;  
 Matches 105; Conservative 0; Mismatches 37; Indels 1; Gaps 1;  
 QY 792 TTAAAGGCTAGTGGCAACCGTCTTTCAGAAATTTGATTTTCAAAAAA 851  
 Db TCTTAAGGCTAGTGGCAACCGTCTTTCAGAAATTTGATTTTCAAAAAA 2929  
 QY 852 TTAGTTATTTCTCTTATTAATAATGAAAAACCTTAGAAAAATGAGTGCAGACTAG 911  
 Db TTAGTTATTTCTCTTATTAATAATGAAAAACCTTAGAAAAATGAGTGCAGACTAG 2989  
 QY 912 CCTTAGAATGTTTTCCCAATPAA 934  
 Db CCTTAGAATGTTTTCCCAATPAA 3012  
 RESULT 13  
 AA15210/c  
 ID AA15210 standard; cDNA; 883 BP.  
 XX  
 XX AA15210;  
 AC  
 XX 07-DEC-2001 (first entry)  
 DT  
 XX

DE Human breast cancer expressed polynucleotide 7667.  
XX Human; breast cancer; cell marker; cytostatic; ss.  
XX Homo sapiens.  
OS WO200151628-A2.  
XX PN  
XX 19-JUL-2001.  
XX PD  
XX 10-JAN-2001; 2001WO-US000798.  
XX PF  
XX 14-JAN-2000; 2000US-0176077P.  
XX PR 14-MAR-2000; 2000US-0189167P.  
XX PR 24-MAR-2000; 2000US-0192099P.  
XX PR 29-MAR-2000; 2000US-0193480P.  
XX PR 15-MAY-2000; 2000US-0205230P.  
XX PR 09-JUN-2000; 2000US-0211315P.  
XX PR 25-JUL-2000; 2000US-0220534P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
XX Lillie J, Xu Y, Wang Y, Steinmann K;  
XX WPI; 2001-451856/48.  
XX  
XX New peptide useful as a marker for the diagnosis of breast cancer.  
XX  
XX Claim 1; Page 1378; 3695pp; English.  
XX  
XX The invention relates to human breast cancer expressed polynucleotides  
CC (AAL07544-AAL26789) and methods of assessing whether a patient is  
CC afflicted with breast cancer by examining the correlation between the  
CC expression of certain markers and the cancerous state of breast cells.  
CC The polynucleotides and encoded polypeptides are potential markers for  
CC detecting, diagnosing, monitoring, characterizing, treating and  
CC potentially preventing breast cancer. The polynucleotides and encoded  
CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity  
XX  
SQ Sequence 883 BP; 322 A; 18 C; 23 G; 396 T; 0 U; 124 Other;  
Query Match 5.4%; Score 70.2; DB 4; Length 883;  
Best Local Similarity 39.2%; Pred. No. 3.9e-05;  
Matches 237; Conservative 0; Mismatches 367; Indels 0; Gaps 0;  
QY 419 TGTCCACTATTGGCACTACCCGAGCAAGATTAAAAAATACCAAGTACTATATCA 478  
DB 873 TGTNNNNNNANACCTAANACCTTTAAANNTNNNNNTTAAANNAANNAATATTTAAANN 814  
QY 479 CTCGAAGCTATCATGTATGTGTTAAAGAAACATCTATTAACACGATCCTTAATAA 538  
DB 813 TANNAATTTTTTNNAAAACTAATTTTAAANNATTAATTTTNNAAAAAANNNAAAAA 754  
QY 539 AACAGCATATTTGCAAGAGACAAATATGTACAGTTTACAAACATCTAAGACGACA 598  
DB 753 TTAANNNTTNTTANTATTAACCAAAATTTTTTTTAAAAAATTTTTTAAANNT 694  
QY 599 AATTTATACGAAGGTAAGCTATGACGTTGAGATTTTCTTTTCAATCTGTATTTTG 658  
DB 633 AATAANTTNAATTTTTTTTAAATNAAAAAATTTTAAATTTTAAACANNTNTTTTT 634  
QY 659 TTATGTTTATATATACATTTTCTCTTACATAGAGTATTTCTTCGATTTTATA 718  
DB 633 TTTNTTNNATTAATAAAAAATTTTAAATTAATAAANNTTTTNTTAAANATTTTAA 574  
QY 719 AAATGACTATAAGTCATTTTATATAAGACGACGATGTCGATGCTCGTCAAAA 778  
DB 573 AAAAAAANNTTTTTTTTTTATANTTTAATAAAAAATTTATTTNTTTCTNAAAAANA 514  
QY 779 TCTTTCTGATTTTTTAAAGAGTATTTGGCAACCTGTTCTTTCAAGAAATTTTGAT 838  
DB 513 AAAAAAATTTTTTAAANNTTTTTTAAACCTTNAATTAANNAANNAATTTTTTNNNT 454

QY 839 TTTTCAAAAAAATTACTTATTTTCTCTTATTAATAAGAAACACTAGAAAAATAGA 898  
DB 453 NNANATTAATAAAATTTATTTTTTTTANTCTATATAATTAATAAANNAATATAAT 394  
QY 899 GTTGCCAGACTAGCCCTAGAGATGTTTCCCAATTAATTAACATCAGTGTATATAT 958  
DB 393 TTTNAAAAAATTAATTTATATNTTANNAANNAANNAATTAATAAANNAATTTTA 334  
QY 959 TGCCAGCCCATTAATTAATTAACCGAAACTGAATCGAGCAACCAATCTGAGCT 1018  
DB 333 NTTAAATTAATAATTAATTAATTAACATTTNTAATTTATTAATTAATAAAAAAAT 274  
QY 1019 ATTT 1022  
DB 273 NTTT 270  
RESULT 14  
ACN85231/C  
ID ACN85231 standard; DNA; 960 BP.  
XX  
XX ACN85231;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Breast cancer related marker, seq id 6381.  
XX  
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; dr.  
XX  
XX Homo sapiens.  
XX OS  
XX US2003099974-A1.  
XX PN  
XX 29-MAY-2003.  
XX PD  
XX 18-JUN-2002; 2002US-00198846.  
XX PF  
XX 18-JUN-2001; 2001US-0306220P.  
XX PR  
XX (MILL-) MILLENNIUM PHARM INC.  
XX PA  
XX Lillie J, Xu Y, Wang Y, Steinmann K;  
XX WPI; 2003-787014/74.  
XX  
XX Novel isolated polypeptide associated with breast cancer, useful for  
XX detecting presence of polypeptide in sample, as a marker for breast  
XX cancer.  
XX  
XX Disclosure; SEQ ID NO 6381; 36pp; English.  
XX  
XX The invention relates to an isolated polypeptide (I) associated with a  
XX breast cancer which is encoded by a nucleic acid molecule comprising a  
XX nucleotide sequence (SI). Further disclosed is an antibody that binds to  
XX the polypeptide of the invention. The activity of the polypeptide of the  
XX invention may be described as cytostatic. The antibody is useful for  
XX detecting the presence of (I) in a sample. Nucleic acid molecules of the  
XX invention are useful in the detection of breast tumours. (I) is useful as  
XX a marker for breast cancer and in breast cancer therapy. Sequences given  
XX in records ACN78851-ACN92934 represent nucleic acid markers associated  
XX with breast cancer. Note: The sequence listing does not form part of the  
XX specification but may be obtained in electronic format from the USPTO web  
XX site at [seqdata.uspto.gov/sequence.html?DocID=2003099974](http://seqdata.uspto.gov/sequence.html?DocID=2003099974)  
XX  
SQ Sequence 960 BP; 340 A; 33 C; 39 G; 421 T; 0 U; 127 Other;  
Query Match 5.4%; Score 70.2; DB 11; Length 960;  
Best Local Similarity 39.2%; Pred. No. 3.9e-05;  
Matches 237; Conservative 0; Mismatches 367; Indels 0; Gaps 0;  
QY 419 TGTCCACTATTGGCACTACCCGAGCAAGATTAAAAAATTAACCAAGTACTATATCA 478

XX WPI; 2004-580996/56.

XX New polynucleotides, specifically nucleic acid fragments encoding

PT flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 (Ap3)

PT homologues, useful for floral development, e.g. engineering plant flowering

PT time.

XX

PS Claim 6; SEQ ID NO 63; 109pp; English.

CC The present invention describes an isolated polynucleotide comprising a

CC first, second, third, fourth or fifth nucleotide sequence, or their

CC complement encoding a polypeptide either having flowering locus T gene

CC (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also

CC described: (1) a vector comprising the polynucleotide; (2) a recombinant

CC DNA construct comprising the polynucleotide; (3) a cell comprising the

CC transforming a cell with the polynucleotide; (4) a cell comprising the

CC recombinant DNA construct; (5) producing a plant comprising transforming

CC a plant cell with the polynucleotide, and regenerating a plant from the

CC transformed plant cell; (6) a plant comprising the recombinant DNA

CC construct; (7) a seed comprising the recombinant DNA construct; (8) an

CC isolated polynucleotide comprising a first nucleotide sequence, where the

CC first nucleotide sequence contains at least 30 nucleotides, and where the

CC first nucleotide sequence is comprised by another polynucleotide, where

CC the other polynucleotide includes the second, third, fourth, fifth or

CC sixth nucleotide sequence; (9) an isolated polypeptide having FT or Ap3

CC homologue activity, as described above; and (10) isolating a polypeptide

CC encoded by the polynucleotide comprising isolating the polypeptide from a

CC cell containing a recombinant DNA construct comprising the polynucleotide

CC operably linked to a regulatory sequence. The polynucleotides are useful

CC for floral development, e.g. engineering plant sterility/fertility,

CC flowering time, plant growth rate, inflorescence architecture, and tissue

CC culture morphology and the rate of cell division to enhance

CC transformation. The present sequence represents an FT homologue

CC nucleotide sequence from the present invention.

XX Sequence 13400 BP; 3962 A; 2948 C; 2695 G; 3795 T; 0 U; 0 Other;

XX

DY Query Match 5.3%; Score 69.8; DB 135; Length 13400;  
Best Local Similarity 73.6%; Pred. No. 9e-05;  
Matches 89; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

XX 811 ACCCTGTTCTTCATCAAGAAATTGGATTGTTCACAAAAAATTAAGTTATTTCTCTTTA 870

DY 8559 ACCATTTTATTTTCAMAGGTTTTTATTTATTAACAAGAAAATTAAGTTCATTTCTCTGG 8618

OY 871 TAAATATGAAGAACCCTTAGAATAATAGAGTTCGCACACTAGCCTCAAGATGTTTTTCCA 930

DY 8619 AAAATATTAATTCATAGAAATAAAGGGGTTCACAACTAGTGCTTTATTAAGTTTCAT 8678/8

OY 931 T 931

DY 8679 T 8679

Search completed: March 5, 2006, 16:11:41  
Job time : 873.437 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 18:11:59 ; Search time 6189.32 Seconds  
(without alignments)  
9910.279 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1\_1311

Perfect score: 1311  
Sequence: 1 ccatggtctctctatgaa.....cgacatcttctctgac 1311

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 2339354228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_hic:\*  
5: gb\_esc4:\*  
6: gb\_esc5:\*  
7: gb\_esc6:\*  
8: gb\_esc7:\*  
9: gb\_esc8:\*  
10: gb\_esc9:\*  
11: gb\_esc10:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	908	69.3	963	9	CC656933 OGMDQ20TM
2	679	51.8	915	10	CG242425 OGAG08TV
3	419.8	32.0	687	9	CC656939 OGMDQ20TV
4	96	7.3	715	10	CG252571 OGAB05TC
5	92	7.0	967	10	CL235046
6	91	6.9	860	10	CZ295176
7	88	6.7	814	10	CG048704
8	87.8	6.7	754	10	CG414922
9	86.6	6.6	950	9	CC439901
10	86.6	6.6	652	9	CC384247
11	86.6	6.6	797	9	CC400575
12	86.6	6.6	820	9	CC400574
13	85.4	6.5	471	10	CG103452
14	85.2	6.5	765	10	CG082135
15	85.2	6.5	781	9	CC630239
16	85.2	6.5	835	10	CC630239
17	85.2	6.5	835	10	CC630239
18	85.2	6.5	835	10	CC630239
19	84.6	6.5	1092	10	CNS020K7
20	84	6.4	793	9	B281381
21	84	6.4	1078	10	CL997678
22	83.8	6.4	530	10	CG201774

C 23	83.6	6.4	722	10	CG333914
C 24	83.6	6.4	722	10	CG333929
C 25	83.6	6.4	781	10	CG034985
C 26	83.6	6.4	861	9	B2797976
C 27	83.6	6.4	865	9	CC430754
C 28	83.6	6.4	861	10	CG102092
C 29	81.8	6.2	947	9	CC435780
C 30	81.8	6.2	981	9	B2784278
C 31	81.8	6.2	1017	9	CC620594
C 32	81.8	6.2	649	9	CC613918
C 33	81.6	6.2	925	9	B2778636
C 34	81.6	6.2	925	10	CG071791
C 35	81.6	6.2	960	9	B2676889
C 36	81.6	6.2	960	9	CC003943
C 37	81.6	6.2	1016	10	CL984151
C 38	81.6	6.2	1022	10	CL984151
C 39	81.4	6.2	999	9	CC385762
C 40	81.2	6.2	756	10	CG221693
C 41	81.2	6.2	1101	10	CNS00L72
C 42	80.6	6.1	792	8	DR794756
C 43	80.6	6.1	699	9	B296930
C 44	80.6	6.1	832	9	CC676387
C 45	80.6	6.1	839	10	CG246849

## ALIGNMENTS

RESULT 1					
LOCUS	CC656933	963 bp	DNA	linear	GSS 19-JUN-2003
DEFINITION	OGMDQ20TM ZM 0.71.5 KB Zea mays genomic clone ZMMB0554D15,				
	genomic survey sequence.				
ACCESSION	CC656933	GI:32060225			
VERSION	CC656933.1				
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
	Var[etia]ntae: Streptophyta: Embryophyta: Tracheophyta:				

REFERENCE  
AUTHORS  
White, J. A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C. M., Budiman, M. A., Bedell, J. A., Rohlfing, T., Citek, R. M., Nurnberg, A., Robbins, D., and Lakey, N.

TITLE  
JOURNAL  
COMMENT  
Unpublished (2002) OTV  
Other\_GSSs: OGMDQ20TV  
Contact: Cathy Whitelaw

TIGR  
712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org

FEATURES  
source  
1. .963  
Location/Qualifiers  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMB0554D15"  
/note="Vector: pBCSK-; Site 1: HindIII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

## ORIGIN

Query Match 69.3%; Score 908; DB 9; Length 963;  
Best Local Similarity 100.0%; Pred. No. 9.6e-180;  
Matches 908; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
404 ACCAGCATTCTAGTCCACTATTGGACCTACCCAGAAAGATTAAAAAATAAC 463

Db	1	ACCGCCATGCTAGTGTGCCACTATGGCACTACCCGACAAAGATTAAAAAATTAACC	60
Qy	464	AAAGTAACTAATTCACATCGAAAGCTATCATGTAATGTTAAAGAAACATCTATTAAAAACC	523
Db	61	AAAGTAACTAATTCACATCGAAAGCTATCATGTAATGTTAAAGAAACATCTATTAAAAACC	120
Qy	524	ACGATCCCTCTAAAAAAACAAGCATATTTGCGAAGAGCAAAATTGTTAGTAGCTTACAA	583
Db	121	ACGATCCCTCTAAAAAAACAAGCATATTTGCGAAGAGCAAAATTGTTAGTAGCTTACAA	180
Qy	584	CATCTAAGAGCGACAAATTATATCGAAAGGTAGCTATGAGCTTCAGATTTTCTTTTC	643
Db	181	CATCTAAGAGCGACAAATTATATCGAAAGGTAGCTATGAGCTTCAGATTTTCTTTTC	240
Qy	644	ATTCTGTATTATTGTTATTTGTTTATATACATTTTCTTCTTACATAGAGTGAATT	703
Db	241	ATTCTGTATTATTGTTATTTGTTTATATACATTTTCTTCTTACATAGAGTGAATT	300
Qy	704	TCTTCGCGATTTTATPAAAATGACATPAAAGTCATTTTATATPAGAGCAGCATGCGTAG	763
Db	301	TCTTCGCGATTTTATPAAAATGACATPAAAGTCATTTTATATPAGAGCAGCATGCGTAG	360
Qy	764	ATTCTCGTCAAAAATCTTCTGATTTTTTTTAAAGCTAGTTGGCAACCCGTGTTCTTT	823
Db	361	ATTCTCGTCAAAAATCTTCTGATTTTTTTTAAAGCTAGTTGGCAACCCGTGTTCTTT	420
Qy	824	CAAGAATTTTGTATTTTTCAAAAAAATTAAGTTATTTTCTCTTTATPAAAATGAAAAAC	883
Db	421	CAAGAATTTTGTATTTTTCAAAAAAATTAAGTTATTTTCTCTTTATPAAAATGAAAAAC	480
Qy	884	ACTTAGAAAAATPAGATGTCGACAGATACCCCTAGATGTTTTTCCCATPAAATTCACATCA	943
Db	481	ACTTAGAAAAATPAGATGTCGACAGATACCCCTAGATGTTTTTCCCATPAAATTCACATCA	540
Qy	944	CTGTGTATPAAATTTATTTGGCCAGCCCCCATPAAATTTATTAACCGAAACTGAAATGAGCGA	1003
Db	541	CTGTGTATPAAATTTATTTGGCCAGCCCCCATPAAATTTATTAACCGAAACTGAAATGAGCGA	600
Qy	1004	AACCAAACTGAGCTATTTCTCTAGTATTAATPAAAAAGGAGAGAGAGAAAGAAATCAG	1063
Db	601	AACCAAACTGAGCTATTTCTCTAGTATTAATPAAAAAGGAGAGAGAGAAAGAAATCAG	660
Qy	1064	TTTTAAGTCATGTCCTCGAGATGTGCGGTTTGGCAAGATAGCCACCGTATCATAGCT	1123
Db	661	TTTTAAGTCATGTCCTCGAGATGTGCGGTTTGGCAAGATAGCCACCGTATCATAGCT	720
Qy	1124	CATAGGTGCTACGTCAGAGTTTGGCAGCTCTGTGTCACTTCACATGGCATCTACATGCG	1183
Db	721	CATAGGTGCTACGTCAGAGTTTGGCAGCTCTGTGTCACTTCACATGGCATCTACATGCG	780
Qy	1184	TTGTTCACACGGTGTGCTGTTCATATCGTCCAAAGCTTGCGCTATCTGAACCAAGAGAT	1243
Db	781	TTGTTCACACGGTGTGCTGTTCATATCGTCCAAAGCTTGCGCTATCTGAACCAAGAGAT	840
Qy	1244	ACCTTACTCCCAAAACAATCATCTTATCTCATGCAAGCTTCATGCAAAACGACATATGTT	1303
Db	841	ACCTTACTCCCAAAACAATCATCTTATCTCATGCAAGCTTCATGCAAAACGACATATGTT	900
Qy	1304	TCCTGAAC 1311	
Db	901	TCCTGAAC 908	

RESULT 2	
CG224225	915 bp DNA linear GSS 22-AUG-2003
LOCUS	
DEFINITION	CG224225 ZM 0.7_1.5 KB Zea mays genomic clone ZMNM8716B15,
ACCESSION	CG224225
VERSION	CG224225.1 GI:34124113
KEYWORDS	GSS.
SOURCE	Zea mays

ORGANISM	Zea mays Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 915)										
REFERENCE	Whitelaw,C.A., Quackenhush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.										
AUTHORS	Consortium for Maize Genomics										
TITLE	Unpublished (2002)										
JOURNAL	Other_GSSS: OGIAG08TH										
COMMENT	Contact: Cathy Whitelaw TIGR										
	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TF Class: methylation filtered. Location/Qualifiers										
FEATURES	1. 915 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone_1db="ZM_0.7.1.5_KB" /note="Vector: pGSK-; Site_1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"										
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Best Local Similarity	99.9%	Pred. No. 9.5e-132;									
Matches 690;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;							
QY	621	TGAGGTCAGATTTTCTTTTCATTCCTGTTATTTGTTATTCGTTTATATACATTTT	680								
DB	1	TGAGGTCAGATTTTCTTTTC-TTCTGTTATTTGTTATTCGTTTATATACATTTT	59								
QY	681	CTTCTCTTACATAGAGTATTTTCTTCGATTTTATTAATAAGTCAATTTT	740								
DB	60	CTTCTCTTACATAGAGTATTTTCTTCGATTTTATTAATAAGTCAATTTT	119								
QY	741	ATATPAAGAGCGGATGCGTGAATTCGCTCAAAAATCTTTCGATTTTTCAGAGC	800								
DB	120	ATATPAAGAGCGGATGCGTGAATTCGCTCAAAAATCTTTCGATTTTTCAGAGC	179								
QY	801	TAGTTGGCAACCGTTCCTTTCAAGAAATTTGATTTTTCAAAAAAATTAAGTTAT	860								
DB	180	TAGTTGGCAACCGTTCCTTTCAAGAAATTTGATTTTTCAAAAAAATTAAGTTAT	239								
QY	861	TTTCTCTTATTAATAAGAAAACTTGAAGAAAAATGAGTTGCCAGACTAGCCTAGAT	920								
DB	240	TTTCTCTTATTAATAAGAAAACTTGAAGAAAAATGAGTTGCCAGACTAGCCTAGAT	299								
QY	921	GTTTTCCTTAATAATTAACAATCTGTGTATAATTTTGGCCAGCCCAATAATTAAT	980								
DB	300	GTTTTCCTTAATAATTAACAATCTGTGTATAATTTTGGCCAGCCCAATAATTAAT	359								
QY	981	AAACCGAAATCGAATCGAGGAAACCAATCTGAGCTATTTCTTAGATTAGTAAAG	1040								
DB	360	AAACCGAAATCGAATCGAGGAAACCAATCTGAGCTATTTCTTAGATTAGTAAAG	419								
QY	1041	GGAGAGAGAGGAAGAAATCAGTTTAACTATGTCCTGAGATGTCGGTTGGCAA	1100								
DB	420	GGAGAGAGAGGAAGAAATCAGTTTAACTATGTCCTGAGATGTCGGTTGGCAA	479								
QY	1101	CGATAGCCACCGTATCATAGCTCATAGGTGCTAGCGTAGGTCGAGCTCTGTGTC	1160								
DB	480	CGATAGCCACCGTATCATAGCTCATAGGTGCTAGCGTAGGTCGAGCTCTGTGTC	539								
QY	1161	ATTCACATGGCATCTACGCTGTTCAACCGTTCGCTTGTTCATCGTCAAGGCT	1220								

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Db      540 ATCTACATGAGCATACATACCTTTGTTCAACGGTTGCTGTTGTCATCTCCAGCTT 599
Qy      1221 TGGCTATTGTAAGAGAGATACCTACCTCCCAAGATCATCTTACATCACTT 1280
Db      600 TGGCTATTGTAAGAGAGATACCTACCTCCCAAGATCATCTTACATCACTT 659
Qy      1281 CATTGCAACACGACATATGTTTCTGAC 1311
Db      660 CATTGCAACACGACATATGTTTCTGAC 690

RESULT 3
CC656939/c 687 bp DNA linear GSS 19-JUN-2003
LOCUS OGM020TV.ZM.0.7.1.5_KB_Zea_mays_genomic_clone_ZMMBma0554D15,
DEFINITION genomic survey sequence.
ACCESSION CC656939
VERSION CC656939.1 GI:32060231
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 687)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Reinick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunez, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSS: OGM020TV
Contact: Cathy White,
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitec@wglr.org
Seq primer: TP
Class: methylation filtered.
Location/Qualifiers
source
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/strain="B73"
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methylation filtered genomic DNA library"

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Best Local Similarity 99.5%; Pred. No. 2e-77; 2; Indels 0; Gaps 0;
Matches 421; Conservative 0; Mismatches 2;

Db      889 GAAATATGAGTTCAGACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 948
Qy      687 GAAATATGAGTTCAGACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 628
Db      949 TATAATATTTGGCCAGCCCATTAATTTTAAACCGAATCGAATCGAAGCA 1008
Qy      627 TATAATATTTGGCCAGCCCATTAATTTTAAACCGAATCGAATCGAAGCA 568
Db      1009 AATCGAGCTATTCTCTAGATTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1068
Qy      567 AATCGAGCTATTCTCTAGATTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 508
Db      1069 AGTCATTTGCTCCGAGATGCGGTTGGCAACGATGACCGATATCATCTCATAG 1128
Qy      507 AGTCATTTGCTCCGAGATGCGGTTGGCAACGATGACCGATATCATCTCATAG 448
Db      1129 GTGCTAGCTAGCTTCCGAGCTCTGCTGATCTCATGATGATCATGATGATCTGTT 1188
Qy      1129 GTGCTAGCTAGCTTCCGAGCTCTGCTGATCTCATGATGATCATGATGATCTGTT 1188

RESULT 4
CG252571/c 715 bp DNA linear GSS 25-AUG-2003
LOCUS O4AB05TC.ZM.0.7.1.5_KB_Zea_mays_genomic_clone_ZMMBma0809B10,
DEFINITION genomic survey sequence.
ACCESSION CG252571
VERSION CG252571.1 GI:34154661
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 715)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Reinick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunez, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy White,
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitec@wglr.org
Seq primer: TP
Class: methylation filtered.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="B73"
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/note="Vector: pBCSK-1; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

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Best Local Similarity 80.1%; Pred. No. 1.5e-09;
Matches 125; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

Db      135 TCTCCACCTCCCGCTGACATTTCTGATGTCGATGTCGATGTCGATGTCGATGTCGAT 194
Qy      356 TCAACACCGCTCTTGTGCTTCTTGATGTCGATGTCGATGTCGATGTCGATGTCGAT 297
Db      195 TCAACACCTCTTGTGCTTCTTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 254
Qy      296 TAAAGCACTGTGAGAACCATTAAGAGCTTTGATGTCGATGTCGATGTCGATGTCGAT 238
Db      255 TCGTGTGATCGAGGATATATGTCCTCCCAATC 290
Qy      237 TCGTGTGATCGAGGATATATGTCCTCCCAATC 202

RESULT 5
CL235046
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LOCUS CL235046 967 bp DNA linear GSS 15-JAN-2004  
DEFINITION ZMMBB0575001r ZMMBB (HindIII) Zea mays genomic clone  
ACCESSION CL235046  
VERSION CL235046.1 GI:40891729  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE 1 (bases 1 to 967)  
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.  
TITLE Sequencing of the maize genome at PCR (2003c)  
JOURNAL Unpublished (2003)  
COMMENT Contact: Bharti,A.K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: SP6  
Class: BAC ends  
High quality sequence start: 64.  
Location/Qualifiers  
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Best Local Similarity 78.6%; Pred. No. 1e-08;  
Matches 110; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 150 TGACATTTCTTGATGCGGTGCTCCATGACGAGGCCCATGACACCTTTGG 209  
DB 827 TGGCCCTTTCTTGATACCGCGGTTCCCTGATTTGAGGCCCATCGACACTTTTGG 886  
QY 210 GACACCATCAAGGCGCTTTGATGCGCCACGAGAGTATCGGCTGTGATCCAGG 269  
DB 887 GTGCGCCATCAAGTCCCTTTGATGTCACAGGAGTATCCGCGCGTGTGACTGGG 946  
QY 270 GGATATATGTCGCCACCAT 289  
DB 947 GGATATCTGTCCCATAGT 966

RESULT 6  
LOCUS CZ295176 860 bp DNA linear GSS 23-MAR-2005  
DEFINITION ZMMBF0063M20f ZMMBF Zea mays genomic clone ZMMBF0063M20 5', genomic  
survey sequence.  
ACCESSION CZ295176  
VERSION CZ295176.1 GI:61708952  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE 1 (bases 1 to 860)  
AUTHORS Bharti,A.K., Nelson,A.B., Young,S., Keizer,G., Zohovetz,V., Fuks,G.  
and Messing,J.  
TITLE Construction, Sequencing and Characterization of a Fosmid library

JOURNAL of the B73 Maize Genome  
COMMENT Unpublished (2005)  
Contact: Bharti,A.K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: Fos F  
Class: fosmid ends  
Location/Qualifiers  
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QY 782 TTCTGATTTTAAAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTTT 841  
DB 51 TTCAAGCACTCTAAGGCTAGTTGACACCTTAATTTTCTAAGAAATTTTATTTT 110  
QY 842 TCAAAAAAATAGTTATTTCTCTTTAATTAATAGAAAAACATTAGAAAAATAGATT 901  
DB 111 TAAAGAAAATAGTTATTTCTCTTGTGAAAATGAAATCCCTTAAAAAATTAAGTT 170  
QY 902 CGCAGACTAGCCCTAGATTTTCCCAATTAATTAATCAATCACTGTGTAATTTTGG 961  
DB 171 ACTAAATTAGCTTTAAAGTTGTTGATGACCACAAAATTAAGATTAAGAGACGA 230  
QY 962 CCAGCCCATTAATTTTAAACGAACAGTAATGAGGAAACCA 1008  
DB 231 GAATCCCTTCTAATGATGAGGGAGAGAAATTCGTAACATATCA 277

RESULT 7  
LOCUS CG048704 814 bp DNA linear GSS 19-AUG-2003  
DEFINITION PULIO19TB ZM\_0\_6\_1.0\_KB Zea mays genomic clone ZMMBTA0611C13,  
genomic survey sequence.  
ACCESSION CG048704  
VERSION CG048704.1 GI:33920884  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE 1 (bases 1 to 814)  
AUTHORS Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,F., Ma,J. and  
Benneetzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: PULIO19TD  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.

FEATURES  
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1. 814  
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Matches 153; Conservative 0; Mismatches 90; Indels 1; Gaps 1;  
QY 713 TTTATTAAGTACTATTAAGTATTTTATTAAGACGACGTCGATTCGCT 772  
DB 487 TTTAAGAGCGTTGAGAGTGAAGATATGAGAAATATCTTTAGAGATGTA 546  
QY 773 CAAAATCTTCTGATTTTATTAAGACTAGTTGGCAACCTGTTCTTCAAGAAAT 832  
DB 547 TAAAGACAGAAACATTTCTTAAGACGATTTGTTTCCATTAATGTAATCGGA 606  
QY 833 TTGATTTTTCAAA-AAAATTAGTTATTTCTCTTATTAATAGAAACCTTAGA 891  
DB 607 TTATCTTCACAGAGGAAAAATGTTATTTCCCTTTGTAATGTAATCGGA 666  
QY 892 AATTAGATGCGACGACGCTAGAGATTTTCCCAATTAATCAATCACTGTGT 951  
DB 667 AATTAGATGCTCAACTAGCCCTAGGTATATCCGATATCCCTATCTCTCT 726  
QY 952 AATT 955  
DB 727 ATT 730

RESULT 8  
CG414922/c 754 bp DNA linear GSS 08-SEP-2003  
LOCUS ZMWBBD0290L09.r ZMWBBD Zea mays genomic clone ZMWBBD0290L09 3'  
DEFINITION genomic survey sequence.  
ACCESSION CG414922  
VERSION CG414922.1 GI:34505144  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 754)  
AUTHORS Lu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.  
and Wang, K.  
TITLE Sequencing of the maize genome  
JOURNAL Unpublished (2003)  
COMMENT Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: T7  
BACKWARD: M13r  
Plate: 0290 row: L column: 09  
Seq primer: M13r  
Class: BAC ends.  
Location/Qualifiers  
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COT selected genomic DNA library"

ORIGIN  
Query Match 6.7%; Score 87.8; DB 10; Length 754;  
Best Local Similarity 71.2%; Pred. No. 7.8e-08;  
Matches 116; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
QY 779 TCTTTCGATTTTATTAAGCTAGTTGGCAACCGTCTTCAAGATTTGAT 838  
DB 680 TCTAATTTTATTTCTTAAGCTAGTTGAAGACACATTTTTCAGAGATTTAT 621  
QY 839 TTTTCAAAAAAATTAAGTTATTTTCTCTTATTAATGAAGACCTTGAAGAAATGA 898  
DB 620 TTTCAATTAATTAATTAATCAATTTTCTTAAGAAATGAAATCAGTGAAGAAATTA 561  
QY 899 GTTGCAGACTAGCCCTAGAAATGTTTCCCAATTAATTAACAT 941  
DB 560 GTTCTTAACCTAACCTTAAGAAATTTCTGTCATTTACAGT 518

RESULT 9  
CC439901/c 950 bp DNA linear GSS 20-MAY-2003  
LOCUS PUHRV15TB ZM\_0\_6\_1.0\_KB Zea mays genomic clone ZMWBTA519D06,  
DEFINITION genomic survey sequence.  
ACCESSION CC439901  
VERSION CC439901.1 GI:30940477  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 950)  
AUTHORS White, C.A., Quackenbush, J., Van Aken, S., Utecher, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Bennetzen, J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUHRV15TD  
Contact: Cathy Whitelaw  
TIGR Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
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Matches 126; Conservative 0; Mismatches 47; Indels 1; Gaps 1;  
QY 787 AATTTCATGAGCTAGTTGGCAACCGTCTTCAAGATTTGATTTTCAAA 846  
DB 241 ATCTTCATGACTAGTTGGCACTATT-TTCACGGGATTTTATTTTCAAT 183

CC400575 797 bp DNA linear GSS 19-MAY-2003  
PHU61TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA480L01,  
genomic survey sequence.

CC400575  
CC400575.1 GI:30880665

GSS.  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 797)  
Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Benner, J.

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PHU61TD  
Contact: Cathy Whiteley

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteley@tigr.org  
Seq primer: TP  
Class: sheared ends.

Location/Qualifiers  
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Cot selected genomic DNA library"

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Best Local Similarity 59.7%; Pred. No. 1,4e-07;  
Matches 163; Conservative 0; Mismatches 109; Indels 1; Gaps 1;

CC400574 820 bp DNA linear GSS 19-MAY-2003  
PHU61TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA480L01,  
genomic survey sequence.

CC400574  
CC400574.1 GI:30880664

GSS.  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 820)  
Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Benner, J.

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PHU61TD  
Contact: Cathy Whiteley

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteley@tigr.org  
Seq primer: TP  
Class: sheared ends.

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Matches 131; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

CC400574 652 bp DNA linear GSS 19-MAY-2003  
PHU61TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA495L13,  
genomic survey sequence.

CC400574  
CC400574.1 GI:30864143

GSS.  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 652)  
Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Benner, J.

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PHU61TD  
Contact: Cathy Whiteley

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteley@tigr.org  
Seq primer: TP  
Class: sheared ends.

Location/Qualifiers  
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/mol\_type="genomic DNA"  
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Cot selected genomic DNA library"

ORIGIN

Query Match 6.6%; Score 86.6; DB 9; Length 652;  
Best Local Similarity 63.9%; Pred. No. 1,4e-07;  
Matches 131; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

CC400574 652 bp DNA linear GSS 19-MAY-2003  
PHU61TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA495L13,  
genomic survey sequence.

CC400574  
CC400574.1 GI:30864143

GSS.  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 652)  
Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Benner, J.

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PHU61TD  
Contact: Cathy Whiteley

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteley@tigr.org  
Seq primer: TP  
Class: sheared ends.

Location/Qualifiers  
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ORIGIN

CC400575 797 bp DNA linear GSS 19-MAY-2003  
PHU61TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA480L01,  
genomic survey sequence.

CC400575  
CC400575.1 GI:30880665

GSS.  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 797)  
Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Benner, J.

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PHU61TD  
Contact: Cathy Whiteley

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteley@tigr.org  
Seq primer: TP  
Class: sheared ends.

Location/Qualifiers  
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Cot selected genomic DNA library"

ORIGIN

Query Match 6.6%; Score 86.6; DB 9; Length 797;  
Best Local Similarity 59.7%; Pred. No. 1,4e-07;  
Matches 163; Conservative 0; Mismatches 109; Indels 1; Gaps 1;

CC400574 820 bp DNA linear GSS 19-MAY-2003  
PHU61TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA480L01,  
genomic survey sequence.

CC400574  
CC400574.1 GI:30880664

GSS.  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 820)  
Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Benner, J.

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PHU61TD  
Contact: Cathy Whiteley

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteley@tigr.org  
Seq primer: TP  
Class: sheared ends.

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Cot selected genomic DNA library"

ORIGIN

Query Match 6.6%; Score 86.6; DB 9; Length 652;  
Best Local Similarity 63.9%; Pred. No. 1,4e-07;  
Matches 131; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

CC400574 652 bp DNA linear GSS 19-MAY-2003  
PHU61TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA495L13,  
genomic survey sequence.

CC400574  
CC400574.1 GI:30864143

GSS.  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 652)  
Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Benner, J.

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PHU61TD  
Contact: Cathy Whiteley

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteley@tigr.org  
Seq primer: TP  
Class: sheared ends.

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Cot selected genomic DNA library"

ORIGIN

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JOURNAL      Unpublished (2003)
COMMENT      Other GSSs: PUBEL19TD
              Contact: Cathy Whitelaw
              TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TP
Class: sheared ends.
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Best Local Similarity 69.5%; Pred. No. 2.4e-07;
Matches 116; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 789 TTTTAAAGCTGCTGTTGGCAACCCGTTCTTCAAGATTTGATTTTTCACAAA 848
Db 216 TTTTCTTAAGCTAGTATGGAATCCATTTTTCACGGATTTATCATTTTTCACAGG 275
QY 849 AATTAATTTATTTTCCTTTTAAATAGAAAACCTTAGAAAAATAGAGTCCGCAGC 908
Db 276 AATTAATGTTCAATTTCTTTGAAAAATAGAAATCAATCGAGAAATAGTGTCCCAAC 335
QY 909 TAGCCCTAGAAATGTTTCCCATTAATATCAATCATCGTGTATTT 955
Db 336 TAGCCCTAGACTTTTCTTAAAAATAGATCAATGAAATTAATTT 382
RESULT 14
LOCUS      CG082135/c
DEFINITION genomic survey sequence.
ACCESSION  CG082135
VERSION    CG082135.1
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM  Zea mays
           Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
           1 (bases 1 to 765)
REFERENCE  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
AUTHORS    Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and
           Benneker,J.
TITLE      Maize Genomics Consortium
JOURNAL    Unpublished (2003)
COMMENT    Other GSSs: PUPX12TB
           Contact: Cathy Whitelaw
           TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TP
Class: sheared ends.
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OY	ATTATTTTAAAGAGCTAGATTGSCAACCCGTTTCTTCAAGAATTTATATTTTCAAA	846
OY	787	
Db	ATCTTTCTAATGACAGTATGTTGGAACTTATTTTCTCAGGATTTTATTTTTCAT	197
OY	847	
Db	AAAAATTAGTTATTTCTCTTATTAATAGAAAACCTTAGAAAAATAGATTGCCAG	906
OY	196	
Db	GAATTTAGTTATTTCTCTTGAGAAAATATTAATCCTTGAGAAAATATAGTTCCAA	137
OY	907	
Db	ACTAGCCCTAGATGTTTTCCCAATTAATTACATCATCTGTGATATATTTTG	960
OY	136	
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RESULT 15				
CC630219/c				
LOCUS	CC630219	781 bp	DNA	linear
DEFINITION	O6GCG33TV ZM 0.7 1.5 KB Zee may's genomic clone ZMMBma0406J09, genomic survey sequence.			

ACCESSION	CC630219	GI:32003354
VERSION	CC630219.1	
KEYWORDS	GSS.	

**SOURCE ORGANISM**

REFERENCE  
AUTHORS  
Mittelbach, C.A., Quackenbush, J., Van Aken, S., Utechtack, T.,

1

TITLE	CONSORTIUM FOR MAIZE GENOMICS
JOURNAL	UNPUBLISHED (2002)
COMMENT	OTHER_GSS: OGU53TH

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel.: 301-878-5843

Tel: 301-838-3843  
 Fax: 301-838-0208

Class: methylation filtered.

## FEATURES

**Source**

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QY 847 AAAAATTAAGTTATTTCTTTATAAAATAGAAAACATTAGAAAATAGAGTTGCAG 906  
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Db 606 GAAATATATTTATTTTCCTGGAGAAATATTAATCATCTGAGAAATATATAGTTCCAA 547

Qy 907 ACTAGCCCTAGATGTTTTCCCAATPAATTCACATCGTGTAATTAATTG 360  
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546 ACTAGCCCTAAGTATTTATTAATTAAGGAAAAATTCGTATTTTCATTG 493

Search completed: March 6, 2006, 01:57:48  
Job time : 6189.32 secs

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93

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model.

Run on: March 5, 2006, 21:54:12 ; Search time 366.534 Seconds  
(without alignments)  
6357.883 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1311	100.0	1394	3	US-08-880-499-1
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4	58.6	4.5	2523	2	US-08-554-467A-1
5	58.6	4.5	2523	2	US-08-410-784A-3
6	57	4.3	19124	3	US-08-487-926B-13
7	56.4	4.3	50000	2	US-08-662-254B-25
8	55.8	4.3	279	3	US-09-312-254A-5297
9	55.8	4.2	612	3	US-09-902-540-1357
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19	53.8	4.1	6027	2	US-08-968-542C-1
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## ALIGNMENTS

RESULT 1  
US-08-880-499-1  
Sequence 1, Application US/08880499  
Patent No. 6037523  
GENERAL INFORMATION:  
APPLICANT: Albertson, Marc C.  
APPLICANT: Fox, Tim W.  
APPLICANT: Carl, Garnat W.  
APPLICANT: Huffman, Gary A.  
APPLICANT: Kendall, Timmy L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION  
TITLE OF INVENTION: AND METHOD OF USING SAME  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESS: PIONEER HI-BRED INTERNATIONAL, INC.  
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.  
CITY: Johnston  
STATE: Iowa  
COUNTRY: USA  
ZIP: 50131  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,499  
FILING DATE: CONCURRENTLY HERewith  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sweeney, Patricia A.  
REGISTRATION NUMBER: 32,733  
REFERENCE/DOCKET NUMBER: 0578  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (515) 248-4840  
TELEFAX: (515) 248-4844  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1394 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-880-499-1  
Query Match 100.0%; Score 1311; DB 3; Length 1394;

Best Local Similarity 100.0%; Pred. No. 8.7e-305;  
Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCAGGAGTCTCTTGAAGAAAGATGAGTACATGTCATATCCGTTTCTTAGGGTCC 60
Db 1 CCAGGAGTCTCTTGAAGAAAGATGAGTACATGTCATATCCGTTTCTTAGGGTCC 60
Qy 61 CTTCTTGCCTTATCTGACATGATCGGGTTACAAAACTTCCAGGGTGCATGAT 120
Db 61 CTTCTTGCCTTATCTGACATGATCGGGTTACAAAACTTCCAGGGTGCATGAT 120
Qy 121 CTCATGTTCCATCTTCCACCTCGGTTGCAATTTCTTGATGTGGTGGTCCAT 180
Db 121 CTCATGTTCCATCTTCCACCTCGGTTGCAATTTCTTGATGTGGTGGTCCAT 180
Qy 181 CTGACCGAGGCCCATCGACACCTTTGGGGACCCCATCAAGGGGCTTGGATGGCCCA 240
Db 181 CTGACCGAGGCCCATCGACACCTTTGGGGACCCCATCAAGGGGCTTGGATGGCCCA 240
Qy 241 CGAAGACGATCGGGTCTGTGATCCAGGGGATATATCTCCCAATCGTCACTATA 300
Db 241 CGAAGACGATCGGGTCTGTGATCCAGGGGATATATCTCCCAATCGTCACTATA 300
Qy 301 TTATTTATCTTTAGATATTTATTTTGGAAAAATACAACTTACTTTTGCTA 360
Db 301 TTATTTATCTTTAGATATTTATTTTGGAAAAATACAACTTACTTTTGCTA 360
Qy 361 GGGGCTCGACATGATTTTCCCTTAGGGCCCAAGAAATGCGAGGACCGACCATGTCTAGT 420
Db 361 GGGGCTCGACATGATTTTCCCTTAGGGCCCAAGAAATGCGAGGACCGACCATGTCTAGT 420
Qy 421 TCCACTATTTGGCACTACCCAGAACAGATTTAAAAATAAACAAGTAACTTCCACT 480
Db 421 TCCACTATTTGGCACTACCCAGAACAGATTTAAAAATAAACAAGTAACTTCCACT 480
Qy 481 CGAAAAGCTATCATGATGTTTAAAGAAACATCTATTTAAACACGATCTCTTAAAAA 540
Db 481 CGAAAAGCTATCATGATGTTTAAAGAAACATCTATTTAAACACGATCTCTTAAAAA 540
Qy 541 CAAGCATTTTTCGAAAGAGACAAATATGTTTACAGTTTACAAACATCTAAGAGGACAA 600
Db 541 CAAGCATTTTTCGAAAGAGACAAATATGTTTACAGTTTACAAACATCTAAGAGGACAA 600
Qy 601 TTAATTCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 TTAATTCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy 661 ATGTTTATATATACATTTTCTCTTCAATAGATGATTTCTCCGATTTATAAA 720
Db 661 ATGTTTATATATACATTTTCTCTTCAATAGATGATTTCTCCGATTTATAAA 720
Qy 721 ATGACTATTAAGATCTTTTATATTAAGAGACGCGATGCTGATTCGTTCAAAAATC 780
Db 721 ATGACTATTAAGATCTTTTATATTAAGAGACGCGATGCTGATTCGTTCAAAAATC 780
Qy 781 TTTCTGATTTTTTAAAGAGTATTTGGCAACCTGTTCTTCAAAAGATTTGATTT 840
Db 781 TTTCTGATTTTTTAAAGAGTATTTGGCAACCTGTTCTTCAAAAGATTTGATTT 840
Qy 841 TTTCAAAAAAATTAATTTATTTCTCTTATTAATAAGAAAACCTTGAATAAGAT 900
Db 841 TTTCAAAAAAATTAATTTATTTCTCTTATTAATAAGAAAACCTTGAATAAGAT 900
Qy 901 TGGCAGACTAGCCCTAGATGTTTCCCAATAAATTAACAATCTGTGTATTAATTTG 960
Db 901 TGGCAGACTAGCCCTAGATGTTTCCCAATAAATTAACAATCTGTGTATTAATTTG 960
Qy 961 GCCAGCCCATTAATTTATTAACGAAATCGAAATCGAGAAACCAATCTGAGCTAT 1020
Db 961 GCCAGCCCATTAATTTATTAACGAAATCGAAATCGAGAAACCAATCTGAGCTAT 1020
Qy 1021 TTTCTAGATTAGTAAAAAGGAGAGAGAGAAATCAATTTTAAAGTATGTGCC 1080
Db 1021 TTTCTAGATTAGTAAAAAGGAGAGAGAGAAATCAATTTTAAAGTATGTGCC 1080
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Db 1021 TTTCTAGATTAGTAAAAAGGAGAGAGAGAAATCAATTTTAAAGTATGTGCC 1080
Qy 1081 TGAGATGCGGTTTGGCAACGATAGCAACCGTATCATATGCTATAGTGGCTAGCTCA 1140
Db 1081 TGAGATGCGGTTTGGCAACGATAGCAACCGTATCATATGCTATAGTGGCTAGCTCA 1140
Qy 1141 GGTTCGACCTCTCGTTCATCTCACATGCGATATCAATGCTTTGTTCAACGTTGCTC 1200
Db 1141 GGTTCGACCTCTCGTTCATCTCACATGCGATATCAATGCTTTGTTCAACGTTGCTC 1200
Qy 1201 TTGTTCCATGCTCAAGCCTTGCCTATTCTGAACCAAGAGATACCTACTCCCAACAAT 1260
Db 1201 TTGTTCCATGCTCAAGCCTTGCCTATTCTGAACCAAGAGATACCTACTCCCAACAAT 1260
Qy 1261 CCATCTTACTCATGCACTTTCATGCAACGACGACATATGTTCTGTAAC 1311
Db 1261 CCATCTTACTCATGCACTTTCATGCAACGACGACATATGTTCTGTAAC 1311
```

## RESULT 2

```
US-08-880-499-2
: Sequence 2, Application US/08880499
: Patent No. 6037523
: GENERAL INFORMATION:
: APPLICANT: Albertson, Marc C.
: APPLICANT: Fox, Tim W.
: APPLICANT: Carl, Garinat W.
: APPLICANT: Huffman, Gary A.
: APPLICANT: Kendall, Jimmy L.
: TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
: NUMBER OF INVENTIONS: 2
: TITLE OF INVENTION: AND METHOD OF USING SAME
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
: STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
: STREET: Box 1000
: CITY: Johnston
: STATE: Iowa
: COUNTRY: USA
: ZIP: 50131
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/880,499
: FILING DATE: CONCURRENTLY HERewith
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Sweeney, Patricia A.
: REGISTRATION NUMBER: 32,733
: REFERENCE/DOCKET NUMBER: 0578
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (515) 248-4800
: TELEFAX: (515) 248-4844
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1394 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-880-499-2
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Query Match 100.0%; Score 1311; DB 3; Length 1394;

Best Local Similarity 100.0%; Pred. No. 8.7e-305;  
Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCAGGAGTCTCTTGAAGAAAGATGAGTACATGTCATATCCGTTTCTTAGGGTCC 60
Db 1 CCAGGAGTCTCTTGAAGAAAGATGAGTACATGTCATATCCGTTTCTTAGGGTCC 60
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QY 61 CTTCTGCGCTTATTAAGCTGAATCGGGGTTTACAAAACTTCAACGGGTGATAT 120  
DB 61 CTTCTGCGCTTATTAAGCTGAATCGGGGTTTACAAAACTTCAACGGGTGATAT 120  
QY 121 CTTCAATGCTGCTTCTCCCACTGCGGTGGAATTTCTGAGTGTGGTTCCTAT 180  
DB 121 CTTCAATGCTGCTTCTCCCACTGCGGTGGAATTTCTGAGTGTGGTTCCTAT 180  
QY 181 CTGACCGAGGCCATCAACACCTTGGGACACCATCATGAGGCTTGGATGGCCCA 240  
DB 181 CTGACCGAGGCCATCAACACCTTGGGACACCATCATGAGGCTTGGATGGCCCA 240  
QY 241 CGAGAGCTATCGGGTGTGTGATCCAGGGGATATATGTCCCAATCGTCACTATA 300  
DB 241 CGAGAGCTATCGGGTGTGTGATCCAGGGGATATATGTCCCAATCGTCACTATA 300  
QY 301 TTATATCTTGTAGATATATTTTATTTTGGAAAAATTAACAACCTATACCTTGTGA 360  
DB 301 TTATATCTTGTAGATATATTTTATTTTGGAAAAATTAACAACCTATACCTTGTGA 360  
QY 361 GGGCTCAGATGATTTTGGCTTAAAGGCGCAAAATGCGAGGACACCATGTCTAGTG 420  
DB 361 GGGCTCAGATGATTTTGGCTTAAAGGCGCAAAATGCGAGGACACCATGTCTAGTG 420  
QY 421 TCCATATGCTGCTACCCAGACAGATTTTAAAAATTAACCAAGTATCTATCTACT 480  
DB 421 TCCATATGCTGCTACCCAGACAGATTTTAAAAATTAACCAAGTATCTATCTACT 480  
QY 481 CGAAGCTATCATGTATGTATTAAGAAACATCTTAAAAACGATCTTTAAAAA 540  
DB 481 CGAAGCTATCATGTATGTATTAAGAAACATCTTAAAAACGATCTTTAAAAA 540  
QY 541 CAAGCATTTTCCAAAGAGACAAATATGTACCTTAAACAACCTTAAAGGACAA 600  
DB 541 CAAGCATTTTCCAAAGAGACAAATATGTACCTTAAACAACCTTAAAGGACAA 600  
QY 601 TTTATTCGAAAGGTAGCTAGATGAGTGGATTTTCTTTTCACTTGTATTTTGT 660  
DB 601 TTTATTCGAAAGGTAGCTAGATGAGTGGATTTTCTTTTCACTTGTATTTTGT 660  
QY 661 ATGTTTATATATCACTTTCTCTCTTACATATAGATTTTCTTCCGATTTTAA 720  
DB 661 ATGTTTATATATCACTTTCTCTCTTACATATAGATTTTCTTCCGATTTTAA 720  
QY 721 ATGACTATTAAGTATTTTATATTAAGAGACGATGTCTGATTTCTGTTCAAAATC 780  
DB 721 ATGACTATTAAGTATTTTATATTAAGAGACGATGTCTGATTTCTGTTCAAAATC 780  
QY 781 TTTCTGATTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGATTTTGAATTT 840  
DB 781 TTTCTGATTTTAAAGCTAGTTGGCAACCTGTTCTTCAAGATTTTGAATTT 840  
QY 841 TTTCAAAAAAATAGTTTATTTCTTCTTAAATAAGAAACCTTGAATAAGAGT 900  
DB 841 TTTCAAAAAAATAGTTTATTTCTTCTTAAATAAGAAACCTTGAATAAGAGT 900  
QY 901 TGGCAGACTAGGCTTGAATTTTCCCAATTAATCAATCTGTGATTAATTTG 960  
DB 901 TGGCAGACTAGGCTTGAATTTTCCCAATTAATCAATCTGTGATTAATTTG 960  
QY 961 GCGAGCCCATTAATTTTAAACCGAACTGAAATCGAGGAAACCAATCTGAGTAT 1020  
DB 961 GCGAGCCCATTAATTTTAAACCGAACTGAAATCGAGGAAACCAATCTGAGTAT 1020  
QY 1021 TTTCTAGATTAAGTAAAGGAGAGAGAGAGAAATACATGTTTAAGTATTTGCC 1080  
DB 1021 TTTCTAGATTAAGTAAAGGAGAGAGAGAGAAATACATGTTTAAGTATTTGCC 1080  
QY 1081 TGAAGATGCGGGTTTGGCAACGATGCGCAACCTGATCATAGTGTCTACCTCA 1140  
DB 1081 TGAAGATGCGGGTTTGGCAACGATGCGCAACCTGATCATAGTGTCTACCTCA 1140  
QY 1141 GGTTCGAGAGCTCTGTGTATCTCAATGAGATCTACATGCTGTTCACACCGTGTGC 1200

DB 1141 GGTTCGAGAGCTCTGTGTATCTCAATGAGATCTACATGCTGTTCACACCGTGTGC 1200  
QY 1201 TGTTCATGCTGCTCAAGGCTTGTCTATTTGAAACCAAGAGATACCTTCCCAACAT 1260  
DB 1201 TGTTCATGCTGCTCAAGGCTTGTCTATTTGAAACCAAGAGATACCTTCCCAACAT 1260  
QY 1261 CCATCTTACTCATGCACTTCCATGCAACGACATATGTTTCTGAAAC 1311  
DB 1261 CCATCTTACTCATGCACTTCCATGCAACGACATATGTTTCTGAAAC 1311  
  
RESULT 3  
US-08-968-542C-1/c  
; Sequence 1, Application US/08968542C  
; Patent No. 5981728  
; GENERAL INFORMATION:  
; APPLICANT: Myers, et al.  
; TITLE OF INVENTION: dult Codes for A No. 5981728el Starch  
; TITLE OF INVENTION: Synchase  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McGregor & Adler, LLP  
; STREET: 8011 Candle Lane  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh  
; SOFTWARE: Microsoft Word 6.0.1 for Macintosh  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/968,542C  
; FILING DATE: No. 5981728ember 12, 1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benjamin Aaron Adler, Ph.D., J.D.  
; REGISTRATION NUMBER: 35,423  
; REFERENCE/DOCKET NUMBER: D6036  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 777-2321  
; TELEFAX: (713) 777-6908  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6027 bp  
; TYPE: nucleic acid  
; STRANDEDNESS: double-stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; DESCRIPTION: cDNA to mRNA  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; ORIGINAL SOURCE:  
; ORGANISM: maize  
; TISSUE TYPE: endosperm  
; IMMEDIATE SOURCE:  
; LIBRARY: maize endosperm cDNA library in  
; LIBRARY: (gt11  
; CLONE: pmg10; pmg6a; pmg6c-2M  
; US-08-968-542C-1  
  
Query Match 5.1%; Score 66.4; DB 2; Length 6027;  
Best Local Similarity 77.5%; Pred.No.5.2e-06;  
Matches 93; Conservative 0; Mismatches 26; Indels 1; Gaps 1;  
  
QY 792 TTTAAGACTAGTGTGGCAACCTGTTCTTTCAAAGATTTTGAATTTTCAAAAAA 851  
DB 5606 TTAAGGCTAGTGTGGCAACCTGTTCTTTCAAAGATTTTGAATTTTCAAAAAA 5548

Qy 852 TTAGTTATTTCTCTTATATAAATAGAAAACACTAGAAAATAGAGTTCCAGACTAG 911  
Db 5547 TTAGTTATTTTTCATTCGTAAGAAAATTTGAAATCTCTTGAGAAAATAGAGTTCCAGACTAG 5488

## RESULT 4

US-09-554-467A-1/c  
Sequence 1, Application US/09554467A  
Patent No. 6639125  
GENERAL INFORMATION:  
APPLICANT: Myers, Alan M.  
APPLICANT: James, Martha G.  
TITLE OF INVENTION: dult Coding for a No. 6639125el Starch Synthase and Uses  
TITLE OF INVENTION: Thereof  
FILE REFERENCE: D6036PCT  
CURRENT APPLICATION NUMBER: US/09/554, 467A  
CURRENT FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: PCT/US98/24225  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 08/062,102  
PRIOR FILING DATE: 1997-11-12  
NUMBER OF SEQ ID NOS: 37  
SEQ ID NO 1  
LENGTH: 6027  
TYPE: DNA  
ORGANISM: maize  
FEATURE: cDNA sequence corresponding to the gene encoding the  
OTHER INFORMATION: starch synthase enzyme DUL.  
US-09-554-467A-1

Query Match 5.1%; Score 66.4; DB 3; Length 6027;  
Best Local Similarity 77.5%; Pred. No. 5.2e-06;  
Matches 93; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

Qy 792 TTTAGAGCTAGTTGGCAACCTGTTCTTTCAAGATTTGATTTTTCAGAAAAA 851  
Db 5606 TCTACGGGCTAGTTGGAGACCCCATTT-TTCCAGAGATTTCCATTTTTCAGAAAAA 5548

Qy 852 TTAGTTATTTCTCTTATATAAATAGAAAACACTAGAAAATAGAGTTCCAGACTAG 911  
Db 5547 TTAGTTATTTTTCATTCGTAAGAAAATTTGAAATCTCTTGAGAAAATAGAGTTCCAGACTAG 5488

## RESULT 5

US-08-410-784A-3/c  
Sequence 3, Application US/08410784A  
Patent No. 5912413  
GENERAL INFORMATION:  
APPLICANT: MYERS, ALAN M.  
APPLICANT: JAMES, MARTHA G.  
TITLE OF INVENTION: ISOLATION OF SU1, A STARCH DEBRANCHING  
TITLE OF INVENTION: ENZYME, THE PRODUCT OF THE MAIZE GENE  
TITLE OF INVENTION: SUGARY 1  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weingarten, Schurgin, Gagnebin and Hayes LLP  
STREET: Ten Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/410,784A  
FILING DATE: 24-MAR-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Heine, Ph.D., Holliday C  
REGISTRATION NUMBER: 34,346  
REFERENCE/DOCKET NUMBER: ISU-002XX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-2290  
TELEFAX: 617-451-0313  
TELEX:

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2523 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-410-784A-3

Query Match 4.5%; Score 58.6; DB 2; Length 2523;  
Best Local Similarity 71.4%; Pred. No. 0.00029;  
Matches 105; Conservative 0; Mismatches 39; Indels 3; Gaps 2;

Qy 774 AAAATCTTCTGATTTTTCAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATT 833  
Db 279 ACATATCATATACATATAATAGGTTAGTTCAGCAATCTTATATCAAAAG--TTT 222

Qy 834 TGATTTTTCAGAAAAATAGTTATTTCTCTTATATAAATAGAAAACACTAGAAA 893  
Db 221 TACATTTTTCAGATAAATAGTTATTTCTCTTGA-AAAATAGAAATTTTCAGAAA 163

Qy 894 ATGAGTTGCCAGACTGACCTAGAAAT 920  
Db 162 ATGAGTTTACAACTAGTCTTAAAT 136

## RESULT 6

US-08-487-826B-13/c  
Sequence 13, Application US/08487826B  
Patent No. 5993827  
GENERAL INFORMATION:  
APPLICANT: Sim, Kim L.  
APPLICANT: Chitnis, Chetan  
APPLICANT: Miller, Louis H.  
APPLICANT: Peterson, David S.  
APPLICANT: Su, Xin-zhaun  
APPLICANT: Welles, Thomas E.  
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe Martens Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,826B  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelien, Ned  
REGISTRATION NUMBER: 29,655

```

? REFERENCE/DOCKET NUMBER: NIM121.001CPT
? TELECOMMUNICATION INFORMATION:
?   TELEPHONE: (619) 235-8550
?   FAX: (619) 235-0176
? INFORMATION FOR SEQ ID NO: 13:
? SOURCE CHARACTERISTICS:
?   LENGTH: 19124 base pairs
?   TYPE: nucleic acid
?   STRANDEDNESS: single
?   TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
US-08-487-826B-13

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Query Match	4.3%;	Score 57;	DB 2;	Length 19124;
Best Local Similarity	50.2%;	Pred. No. 0.0014;		
Matches 141; Conservative	0;	Mismatches 140;	Indels 0;	Gaps 0.

QY	614	TAAAGCAATGAGTTGAGATTTTTCTTTTCATCTGTATATTTGATATGTTTTAAAT	673
Db	15677	TAAATGTTTTTTTTTTCTCTCTGTTTTATTTTTTAAATCAATTTTTTTTTTAAAT	15618
QY	674	ACATTTCTCTCTACATATAGATATTTCTTCGATTTATTAATAAGACATTAAGT	723
Db	15617	AAATATTTTTTTTAATTTTTTTGAAATCTTTTCAATTTTATATCTAATAAATTTTA	15556
QY	734	CATTATTAATAAGACAGCAGTCGTGATATCTCGCAAAAATCTTTCGATTTTT	793
Db	15557	TATTTATATTAATATTTTATATTTTTTTAAATAATTTCTCCTTTTTTTTTTTTTT	15496
QY	794	TAAAGACCTAGTTTGCGAACCCGCTTCTTTCGAAAGATTTGATATTTTTCAAAAAAT	853
Db	15497	TTTTATTTAAATAATTTTTTTTATATATTTCTCTTTTTTTCATTTATTAATTT	15436
QY	854	AGTTTATTTCTCTTATTAATAATGAAAAACCTTGGAAAA	894
Db	15437	GTATTTATATTTCTTTTTTAATAATAAATCAATATATAATAA	15397

RESULT 7  
 US-09-662-254B-26/C  
 Sequence 26, Application US/09662254B  
 Patent No. 6933145  
 GENERAL INFORMATION:  
 APPLICANT: Moyer Richard W.  
 APPLICANT: LI, YI  
 APPLICANT: Banden, Alison Louise  
 TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous  
 TITLE OF INVENTION: Vertebrate Cells  
 FILE REFERENCE: US-221C1X1  
 CURRENT APPLICATION NUMBER: US/09/662,254B  
 CURRENT FILING DATE: 2000-09-14  
 PRIOR APPLICATION NUMBER: 09/086,651  
 PRIOR FILING DATE: 1998-05-29  
 PRIOR APPLICATION NUMBER: 60/224,479  
 PRIOR FILING DATE: 2000-08-10  
 NUMBER OF SEQ. ID NOS: 80  
 SOFTWARE: PatentIn version 3.1  
 SEQ. ID NO. 26  
 LENGTH: 50000  
 TYPE: DNA  
 ORGANISM: *Amsacta moorei* entomopoxvirus  
 US-09-662-254B-26

4.33; Score 56.4; Length 50000;  
 Best Local Similarity 45.11; Pred. No. 0.0026;  
 Matches 257; Conservative 0; Mismatches 306; Indels 7; Gaps 1;

QY 315 ATATATATATATTTTGGAAAAATACAACTTATCTTTGGTGGGCGCTGAGATG 374  
 |||||  
 DB 27972 ATATGATTAACCAATATAAAATTTAAAAATGAAATCAAAATTTATACCTTATATAT 27911

Oy	375	ATTTCGCTTAGGGCCCGAAGAAAGCAGACGACGCATGTCTAGTGTCCACTATTTGGCAC	434
Db	27912	ATTTAAGAAAAAGTGATAATATTATCTGTTGAATTTTAAATTATTAATTATGACATT	27853
Oy	435	TACCAGACAAATTTTTAAAAATATCAACAAGTAATCATCCACTGAAAGCTATCAGT	494
Db	27852	AAATCTTAATCGACACATTAATATATGAGAATTTATTAATTATGAAAAGATTAATGTA	27793
Oy	495	TAAATGTTAAAGAACTCTATTAAGAACGACATCCTCTTAAAAAACAAGCATATTTCCA	554
Db	27792	TBAATATACAAATTAATTTATTAATATACATTAATTAATGTTAAAAATTAAGATTAATTAA	27733
Oy	555	AAGACACAATTTATGTCTACGTTTCAAAACCTGA-----GCGACAATTTATATC	607
Db	27732	ATTAAAGAGAAATTAATTAATTTCAAAGTTTAATATGATATGAAAAATTTATATAA	27673
Oy	608	GAAAGCTAACCTAGACCTCAATTTTCTTTTCATCTGTATTTTGTATGTT	667
Db	27672	TAAATGTTAAAGAAAAATTAATTAATGTTAATATATATGCTACTCTTAAGAAATATGC	27613
Oy	668	TATATACATTTCTCTCTTCAAAAGAGGATTTCTTCGATTTTAAAAATGACTA	727
Db	27612	TTCGATTAATTAATTTAAAGTGGCAAGCTGAATTAATCTCTAGCAATCAAAATT	27553
Oy	728	TAAAGCTATTTAATTAAGAGACGACATGCGATGCTCGTCAAAAATCTTTCGA	787
Db	27552	TAAATTCATCACATAGTCAAGTGAATTTAATATGTTTCTATCGAAAAAGTATATA	27493
Oy	788	TTTTTTAAGACTAGTTGGCAACCTGTTCTTCAAGATTTTGAATTTTTCAAA	847
Db	27492	TATAGATTAAGAAAAATTTAATTAACGATTTATTAAGAAATTTTGAAGATTAABAAAG	27433
Oy	848	AAATATAGTTATTTCTCTTATAAAAA	877
Db	27432	AAAAAGAAATTTATTAATATCACTATACATA	27403

RESULT 8  
 US-09-313-294A-5397  
 Sequence 5397, Application US/09333294A  
 Patent No. 6476212  
 GENERAL INFORMATION:  
 APPLICANT: Lalqudi, Raghunath V.  
 APPLICANT: Ito, Laura Y.  
 APPLICANT: Shetman, Bradley K.  
 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
 FILE REFERENCE: PL-0017 US  
 CURRENT APPLICATION NUMBER: US/09/313,294A  
 CURRENT FILING DATE: 1999-05-14  
 NUMBER OF SEQ ID NOS: 7600  
 SOFTWARE: PERL Program  
 SEQ ID NO 5397  
 LENGTH: 279  
 TYPE: DNA  
 ORGANISM: Zea mays  
 FEATURE:  
 NAME/KEY: misc\_feature  
 OTHER INFORMATION: Inctye ID No. 6476212 700550078H1  
 NAME/KEY: unsure  
 LOCATION: 10, 12, 185-186, 204, 253, 274, 278  
 OTHER INFORMATION: a, t, c, g, or other  
 US-09-313-294A-5397

Query Match 4.3%, Score 55.8; DB 3; Length 279;  
Best Local Similarity 69.0%; Pred. No. 0.0065;  
Matches 89; Conservative 0; Mismatches 39; Indels 1; Gaps 1

0y 789 TTTTAAAGCTACTTTGGCAACCGTGTCTTTCACAAAGATTTTGTATTTTTCACAAA 848  
Db 3 TTTCAANNGCCACTTTTGGAAAAACCCATTTTCCCAAGGGTGTTCATTTTCCCAAGG 62

0y 849 AAATTAGTTATTTTCTCTTTAT-AAATAGAAAAACATAGAAAAATAGAGTCCAGA 907

Db 63 AAGTTAGAACATTTTCCCTTGAGAAATAGAAATCTTTGGGAAATCGAGTTCCCAA 122  
Cy 908 CTAGCCCTA 916  
Db 123 CTAGCCCTA 131

RESULT 9  
US-09-902-540-1357/c  
; Sequence 1357, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1357  
; LENGTH: 612  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(612)  
; OTHER INFORMATION: unsure at all n locations  
US-09-902-540-1357

Query Match 4.2%; Score 55.6; DB 3; Length 612;  
Best Local Similarity 51.4%; Pred. No. 0.00094;  
Matches 127; Conservative 0; Mismatches 120; Indels 0; Gaps 0;  
Cy 626 TTCAGATTTTCTTTTCATTTCTGTATTTTGTATTTGTTATATATACATTTTCTCT 685  
Db 560 TTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 501  
Cy 686 CTACAAATAGAGATTTTCTTCGATTTTATTAAGATTAAGATTAAGATTTTATTA 745  
Db 500 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 441  
Cy 746 AGAGAGCAGTGTAGATCTGTGCAAAATCTTCTGATTTTCTTAAGAGCTAGT 805  
Db 440 ATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 381  
Cy 806 TGGCAACCTGTTCTTCAAGATTTTGAATTTTCAAAAAAATTAATTAATTTCT 865  
Db 380 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 321  
Cy 866 CTTTATA 872  
Db 320 TATTTTA 314

RESULT 10  
US-08-880-499-1/c  
; Sequence 1, Application US/08880499  
; Patent No. 6037523  
; GENERAL INFORMATION:  
; APPLICANT: Albertson, Marc C.  
; APPLICANT: Fox, Tim W.  
; APPLICANT: Carl, Garnat W.  
; APPLICANT: Huffman, Gary A.  
; APPLICANT: Kendall, Timmy L.  
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION  
; TITLE OF INVENTION: AND METHOD OF USING SAME  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.

STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.  
STREET: Box 1000  
CITY: Johnston  
STATE: Iowa  
COUNTRY: USA  
ZIP: 50131  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,499  
FILING DATE: CONCURRENTLY HEREWITH  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sweeney, Patricia A.  
REGISTRATION NUMBER: 32,733  
REFERENCE/DOCKET NUMBER: 0578  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (515) 248-4800  
TELEFAX: (515) 248-4844  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1394 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-880-499-1

Query Match 4.2%; Score 55.6; DB 3; Length 1394;  
Best Local Similarity 55.8%; Pred. No. 0.0012;  
Matches 106; Conservative 0; Mismatches 84; Indels 0; Gaps 0;  
Cy 761 TAGATTCCTGCAAAATCTTTCTGATTTTAAAGAGTAGTTGGCAACCTGTTTC 820  
Db 950 TACACAGATGATGATTTATTTGGAACAACTTACGAGCTAGCTGCAACTATTTT 891  
Cy 821 TTTCAAGAAATTTGATTTTTCAAAAAATTAATTAATTTTCTTTTAAATAGAA 880  
Db 890 TCTAAGCTTTTCTATTTTATTAAGAAATTAACATATTTTGTGAAAAATCAAAA 831  
Cy 881 AACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGATGTTTCCCAATTAATCA 940  
Db 830 TTTCTTGAAGAAACAGAGTTGCCAACTAGCTTTAAAAAATCAAGAAATTTTGA 771  
Cy 941 TCACTGTGA 950  
Db 770 CGAGAACTGA 761

RESULT 11  
US-08-880-499-2/c  
; Sequence 2, Application US/08880499  
; Patent No. 6037523  
; GENERAL INFORMATION:  
; APPLICANT: Albertson, Marc C.  
; APPLICANT: Fox, Tim W.  
; APPLICANT: Carl, Garnat W.  
; APPLICANT: Huffman, Gary A.  
; APPLICANT: Kendall, Timmy L.  
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION  
; TITLE OF INVENTION: AND METHOD OF USING SAME  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.  
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.  
; CITY: Johnston  
; STATE: Iowa  
; COUNTRY: USA  
; ZIP: 50131

Query Match	4.2%	Score 55.6;	DB 3;	Length 1394;
Best Local Similarity	55.8%;	Pred. No. 0.0012;		
Matches 106; Conservative	0;	Mismatches 84;	Indels 0;	Gaps 0;

RESULT 12  
US-09-806-708B-23  
; Sequence 23, Application US/09806708B

Query Match	4.2%	Score 55.4;	DB 3;	Length 1055;
Best Local Similarity	22.5%;	Pred. No. 0.0013;		
Matches 182;	Conservative 181;	Mismatches 430;	Indels 15;	Gaps 3

RESULT 13  
US-09-004-056-1/c  
; Sequence 1, Application US/09004056A

```

1  APPLICANT: Calgene LLC
2  TITLE OF INVENTION: Plant Expansion Promoter Sequences
3  FILE REFERENCE: 125
4  CURRENT APPLICATION NUMBER: US/09/004,056A
5  CURRENT FILING DATE: 1998-01-07
6  EARLIER APPLICATION NUMBER: 60034914
7  EARLIER FILING DATE: 1997-07-01
8  NUMBER OF SEQ ID NOS: 1
9  SOFTWARE: Patentin Ver. 2.0
10 SEQ ID NO 1

```

LENGTH: 2614  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (930)  
; OTHER INFORMATION: unknown nucleotide  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (947)  
; OTHER INFORMATION: unknown nucleotide  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (956)  
; OTHER INFORMATION: unknown nucleotide  
US-09-004-056-1

Query Match 4.2%; Score 55.2; DB 3; Length 2614;  
Best Local Similarity 54.2%; Pred. No. 0.0019;  
Matches 155; Conservative 0; Mismatches 128; Indels 3; Gaps 2;

QY 611 AGTACGATGATGAGTTCAGATTTTCTTTCACTCTGTATTTGTATTTGTTTAA 670  
DB 447 AGTTAGTTGGTATCAATTTTTCATATTAATTTTATTTTCTAAATTTA 388  
QY 671 TATACATTTTCTCTCTACATAGAGTATTTCTCCGATTTTATTAATAAGACTATAA 730  
DB 387 TGTGACAAATGAACCTTATTTATATTTAAATTTATTTGATTAAT-TTTAAAG 329  
QY 731 AGTCATTTTATATAGACACGACATGCTGATGATCTCGTCAAAATCTTCTGATTT 790  
DB 328 TATTTTCAATATATATATTTTCAAGAAAACAATAATTTTCGATTAACGAAATTTTGAGATT 269  
QY 791 TTTTAAAGCATAGTTGGCAACCGTTCTTTCAGAAATTTGATTTTTCAGAAAAA 850  
DB 268 TTTAAATGTAGTATTTTATTTCTTATTTATATCAATAAT-TTATTTAGAAAAA 211  
QY 851 ATTAGTTATTTCTCTTATTAATAAGAAAAACCTTAGAAAAATA 896  
DB 210 ATTAGTTAATGAATTTAAATTTTAAATATTTAAAAAATA 165

RESULT 14  
US-09-640-173-53  
; Sequence 53, Application US/09640173  
; Patent No. 6613515  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND  
; FILE REFERENCE: 210121.484C2  
; CURRENT APPLICATION NUMBER: US/09/640,173  
; CURRENT FILING DATE: 2000-08-15  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 53  
; LENGTH: 396  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(396)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-640-173-53

Query Match 4.2%; Score 55; DB 3; Length 396;  
Best Local Similarity 43.8%; Pred. No. 0.0011;  
Matches 139; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 632 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 691  
DB 11 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 70

QY 692 ATAGAGTATTTCTCCGATTTTATATAAATGACTATTAAGCATTTTATATAGACA 751  
DB 71 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 691  
QY 752 CGCATGCTGATGATCTGCTTCAAAATCTTCTGATTTTATAGCTAGTTGGCAA 811  
DB 131 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 691  
QY 812 CCTGTTCTTCAAGATTTTGAATTTTTCAGAAAAAATAGTATTTCTCTTAA 871  
DB 191 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 691  
QY 872 AAATAGAAAAACCTTAGAAAAATAGAGTTCAGACTAGCCCTAGATTTTCCCAAT 931  
DB 251 AATTCANAAAAAGAAAGAAANATTAANNANNNANNNANNNATNNCTTATATA 310  
QY 932 AAATACATCATCTGTG 948  
DB 311 NTNNNTNNNNNANGGG 327

RESULT 15  
US-09-713-550-53  
; Sequence 53, Application US/09713550  
; Patent No. 6617109  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; FILE REFERENCE: 210121.484C4  
; CURRENT APPLICATION NUMBER: US/09/713,550  
; CURRENT FILING DATE: 2000-11-14  
; NUMBER OF SEQ ID NOS: 205  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 53  
; LENGTH: 396  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(396)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-713-550-53

Query Match 4.2%; Score 55; DB 3; Length 396;  
Best Local Similarity 43.8%; Pred. No. 0.0011;  
Matches 139; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 632 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 691  
DB 11 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 70  
QY 692 ATAGAGTATTTCTCCGATTTTATATAAATGACTATTAAGCTATTTTATAGACA 751  
DB 71 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 691  
QY 752 CGCATGCTGATGATCTGCTTCAAAATCTTCTGATTTTATAGAGTATTTGGCAA 811  
DB 131 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 691  
QY 812 CCTGTTCTTCAAGATTTTGAATTTTTCAGAAAAAATAGTATTTCTCTTAA 871  
DB 191 TTTTCTTTTCATCTGTATTTGTATTTGTTTATATACATTTCTCTTACA 691  
QY 872 AAATAGAAAAACCTTAGAAAAATAGAGTTCAGACTAGCCCTAGATTTTCCCAAT 931  
DB 251 AATTCANAAAAAGAAAGAAANATTAANNANNNANNNANNNATNNCTTATATA 310  
QY 932 AAATACATCATCTGTG 948  
DB 311 NTNNNTNNNNNANGGG 327

Tue Mar 7 10:24:41 2006

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Page 9

Search completed: March 5, 2006, 22:36:25  
Job time : 367.534 secs

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Qy	790	TTTTTAGAGCTAGTTGGCAACCGCTTCTTCGAAGAAATTTGATTTTCAAAAA	84.9
Db	511	TTTATTAGGGCTAATTGTGTAACCACTTT-TTCCAGCGAATTTCAATTTCTTAGAA	56.9
Qy	850	AATTAGTTATTTCTCTTATATAAATAGAAAACCTTAGAAAAATAGAGTGGCAGCT	90.9
Db	570	AATTAGTTAATTTTCGCTTGGGAAATAGAAATTTCAATGGGAAATGCGGTTCCCAACT	62.9
Qy	910	AGCCCTAG	91.7
Db	630	AGCCTTAG	63.7

RESULT 2  
US-10-240-708-36

```

: Sequence 36, Application US/10240708
: Publication No. US20050282157A1
: GENERAL INFORMATION:
: APPLICANT: OLEK, Alexander
: APPLICANT: PIEBENROCK, Christian
: APPLICANT: BEHLIN, Kurt
: TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
: TITLE OF INVENTION: by Assessing DNA Methylation
: FILE REFERENCE: 5013.1012
: CURRENT APPLICATION NUMBER: US/0/240,708
: CURRENT FILING DATE: 2002-10-03
: PRIOR APPLICATION NUMBER: PCT/EP01/03971
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: DE 10019058.8
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: DE 10019173.8
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: DE 10032529.7
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: DE 10043826.1
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 98
: SEQ ID NO 36
: LENGTH: 9347
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
: US-10-240-708-36

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Query Match: 4.4%; Score 57.8; DB 8; Length 9347;

Best Local Similarity 48.9%; Pred. No. 0.64;  
Matches 155; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

Qy	547	TATTTGAAAGAGACAAATTATGTACAGTTTACAAACATCTTAAGAGCGACAAATTATAT	606
Db	8530	TTTTTATTTTGTATGAGAAAGATTTTAAATTTTTTATATATTTAGAGAAATGATTTTTT	8588
Qy	607	CGAAAGTAAAGCTATAGCGTTTCAGATTTTCTTTTTCATTCCTGTATTTTGTATTTGTT	666
Db	8590	AAGATTTTAAATAGAGATTTTGATATATTTTATTTTATTTTGTAGCTTTTGTGTTTGT	8648
Qy	667	TTTATATACATTTCTCTCTTACAAATAGAGATTTTCTCCGATTTATATTAATGCT	726
Db	8650	TATATATTTAAATTTTATAGTTTTTTTTTATATAGATTTTGTTTTGTAAATTTATGTATA	8708
Qy	727	ATTAAGCTATTTTATATATAGAGACGCGATGCGTAGATTCCTGTCAAAATCTTTCG	786
Db	8710	TAAATTTTTTGTGTTTTTTATGAATGTAATGTTTTTTTCGATGTGTTTTTGTGTTTGT	8768
Qy	787	ATTTTTTTAAGAGCTAGTTTGCAACCCGTGTTCTTTCAGAAATTTGATTTTTTCAAA	846
Db	8770	ATGTGTAGTTAAAGAAAGTATATGTTGTTTTTGTGATGTGTAATTTTTTTTTTTTTTTAGA	8828
Qy	847	AAAAATTAGTTATTTT	863
Db	8830	TAAAGATTTATTTTGT	8846

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RESULT 3
US-10-330-773-534
: Sequence 534, Application US/10330773
: Publication No. US20060040282A1
: GENERAL INFORMATION:
: APPLICANT: David W. Morris
: APPLICANT: Marc Malandro
: TITLE OF INVENTION: Novel Compositions and Methods in Cancer
: FILE REFERENCE: 529452001300
: CURRENT APPLICATION NUMBER: US/10/330,773
: CURRENT FILING DATE: 2002-12-27
: NUMBER OF SEQ ID NOS: 981
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 534
: LENGTH: 254396
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-330-773-534

```

Query Match 4.28; Score 55.6; DB 7; Length 254396;

Best Local Similarity 46.2%; Pred. No. 3.3;  
Matches 184; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY	452	AAAAAAAAAACCAAGTAATCTATCCATCTCGAAAGCTATCATGTATGTTTAAAGAAC	511
Db	201251	AAAGAAAAAGAAAGAAAGAAAGAAAGAGAGAGGAGAGAAAGAAAGAAAGAAAGAAAGAA	201310
QY	512	TCTATTTAAACCCAGCATCTCTTTAAAAAACAAGCATATTTGCGAAAGACAATATATGT	571
Db	201311	AAAGAAAAAGAAAGATCTTCTGACAAATATAGGCCATTCATTTGGCCAAACATTTTAGTG	201370
QY	572	ACAGTTTACAAACATCTAGAGCGACAAATATATCGAAAGGTAGCTATGACGTTTCAGA	631
Db	201371	GCTGGCTCGGAATATTTATGACATATTAATTTATCTTTAGTTCAAAACATCTGATTTCAAG	201430
QY	632	TTTTTCTTTTCATCTCTGTATTTTGTATTTGTTTATATATACATTTCTCTCTTAC	691
Db	201431	TTTATCTTTTAAATATTTTACCATTTATTTATCTATATTTTATACTTAAACATATGACTTTT	201490
QY	692	ATAGAGTATTTTCTTCGATTTTATTAATAATGACTATAAGTCAATTTTATATATAAGAGA	751
Db	201491	AAACGTGGGGTTTTTTTTTTCAGCAACCTTAATTAAGAAAGAACAGGTTTACTACAGAGA	201550
QY	752	CGCATGTCGTAGATCTTCGTTCAAAAATCTTTCTGATTTTTTTTAAAGCTAGTTGGCAA	811
Db	201551	AGAACTCAATGGCATTAGATTAGAACAACTCTTAATATCATGAGATTTTTCCTAT	201610
QY	812	CCCTGTTCTTTCAAGAAATTTGATTTTTTCAAAAA	849
Db	201611	TTTGTCAATATTTGATATCATTTTATAGCTTTTTTAAAAA	201648

RESULT 4  
US-09-925-065A-54272

; Sequence 54272, Application US/  
; Publication No. US20040181048A1

; GENERAL INFORMATION:  
; APPLICANT: wang, Da

```

; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;

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; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

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; CURRENT FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-20

; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2000-11-30

; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 54272  
LENGTH: 915  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-54272

Query Match 4.2%; Score 54.8; DB 6; Length 915;  
Best Local Similarity 51.0%; Pred. No. 1.2;  
Matches 151; Conservative 1; Mismatches 143; Indels 1; Gaps 1;

QY ACAATTATATGCAAGGATGAGCTGAGCTGATTTCTTTCTGATTTCTGATTT 655  
DB AAGAT 406  
QY TTGTTATGTTTAT 714  
DB AT 466  
QY TAT 774  
DB TAT 526  
QY AAAATCTTCTGATTTTATATATATATATATATATATATATATATATATAT 834  
DB TAT 586  
QY GATTTTCTGATTTTATATATATATATATATATATATATATATATATATAT 890  
DB TATTTTAT 642

## RESULT 5

US-09-925-065A-803046  
Sequence 803046, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.115  
Nucleotide Polymorphisms in the Human Genome  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 803046  
LENGTH: 488  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-803046

Query Match 4.1%; Score 53.6; DB 6; Length 488;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
Matches 137; Conservative 1; Mismatches 140; Indels 0; Gaps 0;

QY AAGTATGCTATGAGCTGATTTCTTTCTGATTTCTGATTTCTGATTTCTGATTT 669  
DB ATGATGCTGATGCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTT 96  
QY AT 729

DB TTTTATTTTATGAGCTAACTTATGACAGATTTCTTTATATATATATATCTTT 156  
QY AAGTATGCTATGAGCTGATTTCTTTCTGATTTCTGATTTCTGATTTCTGATTT 789  
DB TAACTCTTTTATGCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTT 216  
QY TTTTATGAGCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTT 849  
DB CTGCTCTCTTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTT 276  
QY AATGATTTATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTT 887  
DB TGTCTCTTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTT 314

## RESULT 6

US-10-240-708-73/c  
Sequence 73, Application US/10240708  
Publication No. US20050282157A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
FILE REFERENCE: 5013.1012  
CURRENT APPLICATION NUMBER: US/10/240,708  
PRIOR FILING DATE: 2002-10-03  
PRIOR APPLICATION NUMBER: PCT/EP01/03971  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: DE 10019058.8  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: DE 10032559.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 98  
SEQ ID NO: 73  
LENGTH: 5152  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-240-708-73

Query Match 4.1%; Score 53.6; DB 8; Length 5152;  
Best Local Similarity 48.2%; Pred. No. 3;  
Matches 219; Conservative 0; Mismatches 224; Indels 11; Gaps 2;

QY CTATGAGCTGCTCCAGACAGATTTAAATTAACCAAGTACTATTCCTGCTGAA 484  
DB CTATGAGCTGCTCCAGACAGATTTAAATTAACCAAGTACTATTCCTGCTGAA 4078  
QY AAGTATGCTATGAGCTGATTTCTTTCTGATTTCTGATTTCTGATTTCTGATTT 544  
DB AAGTATGCTATGAGCTGATTTCTTTCTGATTTCTGATTTCTGATTTCTGATTT 4018  
QY CATATTTGAAAGAGCAATATATATATATATATATATATATATATATATATAT 604  
DB TCTCAAAAAAAT 3958  
QY ATGCAAGGATGAGCTGATTTCTTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTT 664  
DB TAT 3898  
QY TTTTAT 723  
DB TATTTTAAATTTTAACTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAACTG 3898  
QY ACTATTAAGCTATTTTATATATATATATATATATATATATATATATATATAT 783



[illegible]

[illegible][illegible]

QY	954	T	954
Db	137018	T	137018

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RESULT 13
US-10-330-773-26
? Sequence 26, Application US/10330773
? Publication NO. US20060040262A1
? GENERAL INFORMATION:
? APPLICANT: David W. Morris
? APPLICANT: Marc Malandro
? TITLE OF INVENTION: Novel Compositions and Methods in Cancer
? FILE REFERENCE: 529452001300
? CURRENT APPLICATION NUMBER: US/10/330,773
? CURRENT FILING DATE: 2002-12-27
? NUMBER OF SEQ ID NOS.: 981
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 26
? LENGTH: 687411
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/feature: misc feature
? LOCATION: (1)..(687411)
? OTHER INFORMATION: n = A,T,C or G
US-10-330-773-26

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Query Match 3.9%; Score 51.2; DB 7; Length 687411;

Matches 170; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

Qy	531	CTTAAAAACAGCATATTTGCAAGAGACAAATTAATGTTCAGTTTCGAACATCTAA	590
Db	98	TATATATATATTAATTTATAGTAAAAATATTTATTAATATATTAATATAAAAATGATAT	157
Qy	591	GAGCACAATATATATCCAAAGGTAGCTATGACGTCAGATTTTCTTTTCATTCTTG	650
Db	158	TATATATATATATATATATATATATATGTAATGTAATTAATATATATATATATATATA	217
Qy	651	TTATTTGTATATGTTTTATATATACATTTTCTTCTTACATATAGATGATTTTCTTCCG	710
Db	218	TATATATATATATTAATTAATATATATAGCATATGTGTAATACATTAATTTTATATATAT	277
Qy	711	ATTTATATAAATGACTATATAGTCATTTTATATATAGACAGCAGATGCTGATTTCTCG	770
Db	278	AGTATAGTAAAT	337
Qy	771	TTCAAAAATCTTTCGATTTTTTTTATAGAGCTATGTCGACCCCTGTTCTTTCTTCAAGAA	830
Db	338	TTTAAAAATGATTTTATATCTTACATATATATTCAAATATATATATATATATATATATA	397
Qy	831	TTTTGATTTTTCAAAAAAATTAGTTATTTTCTCTTATATAAATAGAAAAACATTAGA	890
Db	398	TATATACTTAATAA	457
Qy	891	AAAAATGA 898	
Db	458	TATATAATA 465	

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RESULT 14
US-09-925-065A-667262
/ Sequence 667262, Application US/09925065A
/ Publication No. US2004018104A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925.065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096

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RESULT 15  
US-09-925-065A-667263  
Sequence 667263, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
File Reference: 108927.135  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/243, 096  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/252, 147  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/250, 092  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/261, 766  
PRIOR FILING DATE: 2001-01-16

Search completed: March 6, 2006, 10:32:49  
Job time : 1371.54 secs

**THIS PAGE BLANK (USPTO)**

Query Match	100.0%;	Score 1311;	DB 8;	Length 1394;
Best Local Similarity	100.0%;	Fret-No. 6,282-275;		
Matches 1311;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	CCATGGTGTCTCTATGAAAAGAAATGATCATATGTGCTATATATCGTTTCTTAAAGGCC	60	
Db	1	CCATGGTGTCTCTAGAAAAGAAATGATCATATGTGCTATATATCGTTTCTTAAAGGCC	60	
QY	61	CTTCTTTCGCTCTATTATCTGATCTGAAATCGGGGTTTCAAAAACCTTCACGGGTCATAT	120	
Db	61	CTTCTTTCGCTCTATTATCTGATCTGAAATCGGGGTTTCAAAAACCTTCACGGGTCATAT	120	
QY	121	CTTCATATCTCACTTTCGCCACCTCGTGGTTGACATTTCTTGAGATGTGGTGTCCCAT	180	
Db	121	CTCATATCTCACTTCTCCACCTCGGTTGACATTTCTTGAGATGTGGTGTCCCAT	180	
QY	181	CTGACCGAGGCGCATACAGACACCTTTGGGACACCCATCAAGGGGCTTTGGATGGGCCA	240	
Db	181	CTGACCGAGGCGCATACAGACACCTTTGGGACACCCATCAAGGGGCTTTGGATGGGCCA	240	
QY	241	CGAGACGATATCGGGTCGTGGATCAAGGAGATATATGCCCCCAATGTCACCTATA	300	

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|||||
Db 241 CGAGACGATCGGCTCGTGATCCAGGGGATATATGCCCCCAATCGTCACCTATA 300
Qy 301 TTATATCTCTTAACTATATATATATATATATATATATATATATATATATATATAT 360
Db 301 TTATATCTCTTAACTATATATATATATATATATATATATATATATATATATATAT 360
Qy 361 GGGGCTCAGCATATATTTGGCTTAGGGCCAGAAATGCGAGACCAAGCATGTCTAGTG 420
Db 361 GGGGCTCAGCATATATTTGGCTTAGGGCCAGAAATGCGAGACCAAGCATGTCTAGTG 420
Qy 421 TCCACTATGGCACTACCGAGACCAAGATTTAAAAAATACCAAGTAACTATCCACT 480
Db 421 TCCACTATGGCACTACCGAGACCAAGATTTAAAAAATACCAAGTAACTATCCACT 480
Qy 481 CGAAGCATCATATATATATATATATATATATATATATATATATATATATATATAT 540
Db 481 CGAAGCATCATATATATATATATATATATATATATATATATATATATATATATAT 540
Qy 541 CAAGCATATTTGAAAGAGACAAATATATATATATATATATATATATATATATATAT 600
Db 541 CAAGCATATTTGAAAGAGACAAATATATATATATATATATATATATATATATATAT 600
Qy 601 TTATATCGAAGGTAAGCTATGACGTTCAATTTTCTTTTCAATCTGTATTTGTT 660
Db 601 TTATATCGAAGGTAAGCTATGACGTTCAATTTTCTTTTCAATCTGTATTTGTT 660
Qy 661 ATTGTTTTTATATATATATATATATATATATATATATATATATATATATATATAT 720
Db 661 ATTGTTTTTATATATATATATATATATATATATATATATATATATATATATATAT 720
Qy 721 ATGACTATATATATATATATATATATATATATATATATATATATATATATATAT 780
Db 721 ATGACTATATATATATATATATATATATATATATATATATATATATATATATAT 780
Qy 781 TTTCTGATTTTTTAAAGCTAGTTGGCAACCGTGTCTTTTCAAGATTTTGAATTT 840
Db 781 TTTCTGATTTTTTAAAGCTAGTTGGCAACCGTGTCTTTTCAAGATTTTGAATTT 840
Qy 841 TTTCAAAAAAATATGTTATATTTCTCTTATATATATATATATATATATATATAT 900
Db 841 TTTCAAAAAAATATGTTATATTTCTCTTATATATATATATATATATATATATAT 900
Qy 901 TGCCAGACTAGCCCTAGATGTTTTCCCAATTAATCACTAGTGTATATATATTTG 960
Db 901 TGCCAGACTAGCCCTAGATGTTTTCCCAATTAATCACTAGTGTATATATATTTG 960
Qy 961 GCCAGCCCCATTAATTTATTAACCGAAATCGAATCGAGGAAACCAATCTGAGCTAT 1020
Db 961 GCCAGCCCCATTAATTTATTAACCGAAATCGAATCGAGGAAACCAATCTGAGCTAT 1020
Qy 1021 TTTCTATATATATATATATATATATATATATATATATATATATATATATATAT 1080
Db 1021 TTTCTATATATATATATATATATATATATATATATATATATATATATATATAT 1080
Qy 1081 TGAAGTGTGCGGTTTGGCAAGATGCAACCGTATATCACTAGTGTATATATATAT 1140
Db 1081 TGAAGTGTGCGGTTTGGCAAGATGCAACCGTATATCACTAGTGTATATATATAT 1140
Qy 1141 GGTTCGCGAGCTCTGTGTCACTCAATGCGATATCAATGCTTTGCAACCGTTGTC 1200
Db 1141 GGTTCGCGAGCTCTGTGTCACTCAATGCGATATCAATGCTTTGCAACCGTTGTC 1200
Qy 1201 TTTGTTCAATGCTTCAAGGCTTGGCCTATCTGAACCAAGATATCTTCTCCAAACAT 1260
Db 1201 TTTGTTCAATGCTTCAAGGCTTGGCCTATCTGAACCAAGATATCTTCTCCAAACAT 1260
Qy 1261 CCATCTTATCATGCACTTCCATGCAACGACATATATGTTTCTGTAAAC 1311
Db 1261 CCATCTTATCATGCACTTCCATGCAACGACATATATGTTTCTGTAAAC 1311
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RESULT 2

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US-10-713-381-2
; Sequence 2, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAT, CARL W.
; APPLICANT: HOFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-2

Query Match 100.0%; Score 1311; DB 8; Length 1394;
Best Local Similarity 100.0%; Pred. No. 6,2e-275; Indels 0; Gaps 0;
Matches 1311; Conservative 0; Mismatches 0;

Qy 1 CCATGAGTCTCTATGAAAAAGATGAGTACATGTGCTATATCCGTTTCTTAGGGTCC 60
Db 1 CCATGAGTCTCTATGAAAAAGATGAGTACATGTGCTATATCCGTTTCTTAGGGTCC 60
Qy 61 CTTCCTGCTTATATATATATATATATATATATATATATATATATATATATATATAT 120
Db 61 CTTCCTGCTTATATATATATATATATATATATATATATATATATATATATATATAT 120
Qy 121 CTCATGTTCCACTTCTCCCACTCGGCTTGACATTTCTTGATGTGCTGTCCCAT 180
Db 121 CTCATGTTCCACTTCTCCCACTCGGCTTGACATTTCTTGATGTGCTGTCCCAT 180
Qy 181 CTGACGAGGCCATTCAGACACCTTTGGGACACCCATCAAGGGCTTTGGATGGCCCA 240
Db 181 CTGACGAGGCCATTCAGACACCTTTGGGACACCCATCAAGGGCTTTGGATGGCCCA 240
Qy 241 CGAGACGATCGGGTCGTGTGATCCAGGGATATATGTCCCCCAATGCTACCTATA 300
Db 241 CGAGACGATCGGGTCGTGTGATCCAGGGATATATGTCCCCCAATGCTACCTATA 300
Qy 301 TTATATCTCTTAACTATATATATATATATATATATATATATATATATATATATAT 360
Db 301 TTATATCTCTTAACTATATATATATATATATATATATATATATATATATATATAT 360
Qy 361 GGGGCTCAGCATATATTTGGCTTAGGGCCAGAAATGCGAGACCAAGCATGTCTAGTG 420
Db 361 GGGGCTCAGCATATATTTGGCTTAGGGCCAGAAATGCGAGACCAAGCATGTCTAGTG 420
Qy 421 TCCACTATGGCACTACCGAGACCAAGATTTAAAAAATACCAAGTAACTATCCACT 480
Db 421 TCCACTATGGCACTACCGAGACCAAGATTTAAAAAATACCAAGTAACTATCCACT 480
Qy 481 CGAAGCATCATATATATATATATATATATATATATATATATATATATATATATAT 540
Db 481 CGAAGCATCATATATATATATATATATATATATATATATATATATATATATATAT 540
Qy 541 CAAGCATATTTGAAAGAGACAAATATATATATATATATATATATATATATATATAT 600
Db 541 CAAGCATATTTGAAAGAGACAAATATATATATATATATATATATATATATATATAT 600
Qy 601 TTATATCGAAGGTAAGCTATGACGTTCAATTTTCTTTTCAATCTGTATTTGTT 660
Db 601 TTATATCGAAGGTAAGCTATGACGTTCAATTTTCTTTTCAATCTGTATTTGTT 660
Qy 661 ATTGTTTTTATATATATATATATATATATATATATATATATATATATATATATAT 720
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Query	Seq	Score	Length	Mismatches	Indels	Gaps
1145	CGGAGAGCTGCTGTCATCTCAATGAGATACATGCTTTGTTCAACCGTTCGTCCTGT	1204				
Db	5	CGGAGATCCCGTTCATCTCAATGAGATACATGCTTTGTTCAACCGTTCGTCCTGT	64			
Query	1205	TCGATCGTCGCAAGCTTGGCTATTCGTAAACGAAGATACCTACTCCCAACATTCAT	1264			
Db	65	TCGATCGTCGCAAGCTTGGCTATTCGTAAACGAAGATACCTACTCCCAACATTCAT	124			
Query	1265	CTTACTGATGCAACTTCGATGCAACGAGATATGTTCTCGAAC	1311			
Db	125	CTTACTGATGCAACTTCGATGCAACGAGATATGTTCTCGAAC	171			

  

Query	Seq	Score	Length	Mismatches	Indels	Gaps
1155	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	1213				
Db	1	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	60			
Query	1214	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	1273			
Db	61	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	120			
Query	1274	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	1311			
Db	121	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	158			

  

Query	Seq	Score	Length	Mismatches	Indels	Gaps
1158	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	1213				
Db	1	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	60			
Query	1214	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	1273			
Db	61	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	120			
Query	1274	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	1311			
Db	121	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	158			

  

Query	Seq	Score	Length	Mismatches	Indels	Gaps
1158	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	1213				
Db	1	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	60			
Query	1214	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	1273			
Db	61	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	120			
Query	1274	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	1311			
Db	121	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	158			

  

Query	Seq	Score	Length	Mismatches	Indels	Gaps
1158	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	1213				
Db	1	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	60			
Query	1214	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	1273			
Db	61	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	120			
Query	1274	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	1311			
Db	121	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	158			

  

Query	Seq	Score	Length	Mismatches	Indels	Gaps
1158	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	1213				
Db	1	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	60			
Query	1214	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	1273			
Db	61	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	120			
Query	1274	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	1311			
Db	121	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	158			

  

Query	Seq	Score	Length	Mismatches	Indels	Gaps
1158	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	1213				
Db	1	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	60			
Query	1214	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	1273			
Db	61	CAAGCTTGGCTATTTCTGAACCAAGGATACCTACTCCCAACATTCATTTACTCAT	120			
Query	1274	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	1311			
Db	121	GCAACTTCGATGCAACGACGACATATGTTCTCGAAC	158			

  

Query	Seq	Score	Length	Mismatches	Indels	Gaps
1158	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	1213				
Db	1	CGTGTCACTTCGACATGGGATACCTACATGCTTTGTTCAACCGTTCGTC	60			

ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_53903C.1  
US-10-425-115-134230

Query Match  
Best Local Similarity 78.2%; Pred. No. 3.9e-07;  
Matches 97; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 792 TTTAAGGCTAGTGTGGCAACCCGTTCTTCAAGATTGATTTTCAAAAAA 851  
DB 999 TCTTAAGGCTAGTGTGGCAACCTTATTTTAAAGATTCTTTTAAAGATAA 1058  
QY 852 TTAGTTATTTCTCTTATTAATAAGAAAACCTTAGAAAATAGAGTTGCCAGACTAG 911  
DB 1059 TTAGTTATTTCTCTTGAAGAAAATAGAAATCTGTGAAAATTTGAGTTGCTAACTAG 1118  
QY 912 CCCT 915  
DB 1119 CCCT 1122

#### RESULT 6

US-10-425-114-23340  
Sequence 23340, Application US/10425114  
Publication No. US20040034888A1

GENERAL INFORMATION:  
APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(5313)B  
CURRENT APPLICATION NUMBER: US/10/425.114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 23340  
LENGTH: 320  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3595-039-G8\_FLI  
US-10-425-114-23340

Query Match  
Best Local Similarity 73.1%; Pred. No. 6e-06;  
Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 791 TTTAAGGCTAGTGTGGCAACCCGTTCTTCAAGATTGATTTTCAAAAAA 850  
DB 62 TTTTAAAGGCTAGTGTGGCAACCTTATTTTCAAGATTGATTTTCAAGAA 121  
QY 851 ATTAGTTATTTCTCTTATTAATAAGAAAACCTTAGAAAATAGAGTTGCCAGACTA 910  
DB 122 ATTAGTTATTTCTCTTGAAGAAAATAGAAATCTGTGAAAATTTGAGTTGCTAACTAG 181  
QY 911 GCCCTAGAT 920  
DB 182 GCCCTAATT 191

#### RESULT 7

US-10-425-114-16264  
Sequence 16264, Application US/10425114  
Publication No. US20040034888A1

GENERAL INFORMATION:  
APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(5313)B  
CURRENT APPLICATION NUMBER: US/10/425.114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 16264  
LENGTH: 624  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3062-023-G10\_FLI  
US-10-425-114-16264

Query Match  
Best Local Similarity 73.1%; Pred. No. 8.3e-06;  
Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 791 TTTAAGGCTAGTGTGGCAACCCGTTCTTCAAGATTGATTTTCAAAAAA 850  
DB 374 TTTTAAAGGCTAGTGTGGCAACCTTATTTTCAAGATTGATTTTCAAGAA 433  
QY 851 ATTAGTTATTTCTCTTATTAATAAGAAAACCTTAGAAAATAGAGTTGCCAGACTA 910  
DB 434 ATTAGTTATTTCTCTTGAAGAAAATAGAAATCTGTGAAAATTTGAGTTGCTAACTAG 493  
QY 911 GCCCTAGAT 920  
DB 494 GCCCTAATT 503

#### RESULT 8

US-10-425-115-141826  
Sequence 141826, Application US/10425115  
Publication No. US20040214272A1

GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(5322)B  
CURRENT APPLICATION NUMBER: US/10/425.115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 141826  
LENGTH: 1326  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_60829C.1  
US-10-425-115-141826

Query Match  
Best Local Similarity 69.1%; Pred. No. 2e-05;  
Matches 114; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

QY 756 TGTCGTAGATTCGTCGCAAAAATCTTCTGATTTTAAAGACTAGTTGGCAACCT 815  
DB 1090 TGAAGTTGGTGTGTGTGTGATTTCACTTAACTGAAGACTAATTTGGGAACCA 1149  
QY 816 GTTCTTTCAAGAAATTTGATTTTCAAAAAAATAGTTATTTCTTTATATAA 875  
DB 1150 ATTT-TTCCACTGATTTTCATTTTCTTAAGAAAATAGTTTCCCTTGAGAAA 1208  
QY 876 TAGAAAACCTTAGAAAATAGAGTTGCCAGACTAGCCCTAGAT 920  
DB 1209 TAGAATCTTAGAAAATAGAGTTGCCAGACTAGCCCTAAT 1253

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RESULT 10
US-10-425-115-83293/c
Sequence 83293, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongqei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ. ID NOS: 369326
SEQ. ID NO. 83293
LENGTH: 2729
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(2729)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: M14577_175978C.1
US-10-425-115-83293
Query Match 5.6%; Score 72.8; DB 8; Length 2729;
Best Local Similarity 60.7%; Pred. No. 3, 1e-05;
Matches 116; Conservative 0; Mismatches 87; Indels 1; Gaps 1;

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[illegible]

;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(5313)B  
;; CURRENT APPLICATION NUMBER: US/10/425,114  
;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 73128  
;; SEQ ID NO 17816  
;; LENGTH: 928  
;; TYPE: DNA  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: LIB3075-032-A3\_FLI  
US-10-425-114-17816

Query Match 5.5%; Score 71.8; DB 7; Length 928;  
Best Local Similarity 78.0%; Pred. No. 3e-05;  
Matches 99; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

Qy 790 TTTTAAAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTTTCAAAAAA 849  
Db 804 TTTTAAAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTTTCAAAAAA 746  
Qy 850 AATTAGTTATTTCTCTTATTAATAATAGAAACCTAGAAATAGAGTTCAGACT 909  
Db 745 AATTAGTTATTTCTCTTATTAATAATAGAAATAGTCTTGAAAAATAGAGTTCAGAAATT 686  
Qy 910 AGCCCTA 916  
Db 685 ACCCCTA 679

RESULT 13  
US-10-425-115-142853/C  
; Sequence 142853, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 142853  
; LENGTH: 1123  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_61761C.1  
US-10-425-115-142853

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Db 762 AATTAGTTATTTCTCTTATTAATAATAGAAATAGTCTTGAAAAATAGAGTTCAGAAATT 703  
Qy 910 AGCCCTA 916  
Db 702 ACCCCTA 696

RESULT 14  
US-10-425-114-31957  
; Sequence 31957, Application US/10425114

;; Publication No. US20040034888A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Liu, Jingdong  
;; APPLICANT: Zhou, Yihua  
;; APPLICANT: Kovalic, David K.  
;; APPLICANT: Screen, Steven B  
;; APPLICANT: Tabaska, Jack E  
;; APPLICANT: Cao, Yongwei  
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
;; FILE REFERENCE: 38-21(5313)B  
;; CURRENT APPLICATION NUMBER: US/10/425,114  
;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 73128  
;; SEQ ID NO 31957  
;; LENGTH: 2537  
;; TYPE: DNA  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: UC-2MFLB73238H12\_FLI  
US-10-425-114-31957

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Matches 105; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

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Db 1858 TTAGTTATTTCTCTTATTAATAATAGAAATAGTCTTGAAAAATAGAGTTCAGAACTAG 1917  
Qy 912 CCTAGAAATTTTCCCAATAA 934  
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; Sequence 52216, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
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US-10-425-115-52216

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Db 1918 CCTTAATGTTTTTTTCATGAA 1940  
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Run on: March 5, 2006, 17:38:03 ; Search time 685.165 Seconds  
(without alignments)

13025.213 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapen 10.0 Gapext 1.0

Searched: 5883141 seqs, 28421725653.residues

Total number of hits satisfying chosen parameters: 11766282

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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5	157	100.0	1394	6	AX224395	Sequence
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16	33.8	21.5	214178	5	BX640577	Zebrafish
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REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
1	Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.	Male tissue-preserved regulatory region and method of using same	Patent: WO 0160997-A 9 23-AUG-2001;	PIONEER HI-BRED INTERNATIONAL, INC. (US)	Location/Qualifiers 1..255 1..255

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OY	61	AAGCCTTGCCATTTCTGTAACCAAGAGATCTCTATCCCAAAATGCACTTATCTCATG	120
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VERSION JP 2001520523-A/1.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 1394)  
Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and  
Kendall,T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL PIONEER HI BRED INTERNATIONAL INC  
PATENT: JP 2001520523-A 1 30-OCT-2001;  
PIONEER HI BRED INTERNATIONAL INC  
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ACCESSION BD062177.1 GI:22607782  
VERSION JP 2001520523-A/2.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 1394)  
Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and  
Kendall,T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL PIONEER HI BRED INTERNATIONAL INC  
PATENT: JP 2001520523-A 2 30-OCT-2001;  
PIONEER HI BRED INTERNATIONAL INC  
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PD 30-OCT-2001  
PF 19-JUN-1998 JP 199504910  
PR 23-JUN-1997 US 08/880499  
PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAAT,GARY A HUFFMAN,  
TIMMY L KENDALL  
PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC  
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DB 1215 AAGCTTGCCCTATCTGTAACCAAGAGATCTACTCCCAAAACATCATCTTACTCATG 1274  
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DB 1275 CAACCTTCATGCAAAACGACGACATATGTTCTCTGAC 1311  
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LOCUS Sequence 1 from Patent WO0160997.  
DEFINITION  
ACCESSION AX224394  
VERSION AX224394.1 GI:15554636  
KEYWORDS Zea mays  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1  
Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)  
FEATURES  
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QY 61 AAGCTTGCCCTATCTGTAACCAAGAGATCTACTCCCAAAACATCATCTTACTCATG 120  
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QY 121 CAACCTTCATGCAAAACGACGACATATGTTCTCTGAC 157

Db 1275 CAACCTTCAGCAAAACGACACATATGTTCTCTGAC 1311

RESULT 5  
LOCUS AX224395 1394 bp DNA linear PAT 10-SEP-2001  
DEFINITION Sequence 2 from Patent WO0160997.  
ACCESSION AX224395  
VERSION AX224395.1 GI:15554637  
KEYWORDS  
SOURCE  
ORGANISM  
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS 1 Albertsen, M.C., Fox, T.W., Garnat, C.W., Huffman, G. and Kendall, T.L.  
JOURNAL Male tissue-preferred regulatory region and method of using same  
Patent: WO 0160997-A 2 23-AUG-2001  
PIONEER HI-BRED INTERNATIONAL, INC. (US)  
LOCATION/Qualifiers  
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DEFINITION Zea mays male fertility protein (Ms45) gene, complete cds.  
ACCESSION AF360356  
VERSION AF360356.1 GI:14028756  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS 1 (bases 1 to 3343)  
JOURNAL Fox, T.W., Trimmell, M.R. and Albertsen, M.C.  
TITLE Cloning of Ms45, a gene required for male fertility from Zea mays  
REFERENCE 2 (bases 1 to 3343)  
AUTHORS Fox, T.W., Trimmell, M.R. and Albertsen, M.C.  
JOURNAL Direct Submission  
TITLE Submitted (13-MAR-2001) Trait and Technology Development, Pioneer  
H1-Bred Intl, Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,  
IA 50131-1004, USA  
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Qy 121 CACTTCATGCAAAACGACACATATGTTCTCTGAC 157  
Db 1275 CAACCTTCAGCAAAACGACACATATGTTCTCTGAC 1311

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VERSION AX224396.1 GI:15554638  
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ORGANISM  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS 1 Albertsen, M.C., Fox, T.W., Garnat, C.W., Huffman, G. and Kendall, T.L.  
JOURNAL Male tissue-preferred regulatory region and method of using same  
Patent: WO 0160997-A 3 23-AUG-2001  
PIONEER HI-BRED INTERNATIONAL, INC. (US)  
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Query Match	34.4%	Score 54;	DB 15;	Length 110000;
Best Local Similarity	85.7%	Pred. No. 1.8e-06;		
Matches	60;	Conservative	0;	Mismatches 10;
		Indels	0;	Gaps
			0;	

  

QY	64	CTTGGCTATTCTGAACGAAAGGATCTCTACTCCCAACATCCATCTTACTCATGCA	123
Db	36362	CTTGGCTATTCTGAACGAAAGGATCTCTACTCCCAACATCCATCTTACTCATGCA	36303
QY	124	CTTCCATGCA	133

  

Db	36302	CTTCCATGCA	36293
RESULT	9		
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LOCUS	AC135206		
DEFINITION	Oryza sativa (japonica cultivar-group) chromosome 3 clone		
ACCESSION	AC135206		
VERSION	AC135206.3		
KEYWORDS	HTG.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE	Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Currie,J. and Collura,K.		
TITLE	Rice Genomic Sequence		
JOURNAL	Unpublished		
AUTHORS	Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Sasaki,C., Currie,J., Collura,K. and Thompson,S.		
TITLE	Direct Submission		
REFERENCE	Submitted (09-OCT-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA		
AUTHORS	Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Currie,J., Collura,K. and Thompson,S.		
TITLE	Direct Submission		
REFERENCE	Submitted (06-NOV-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA		
AUTHORS	Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Currie,J., Collura,K. and Thompson,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-JAN-2003) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA		
REFERENCE	Submitted (16-APR-2003) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA		
AUTHORS	On Jan 11, 2003 this sequence version replaced gi:24635891.		
TITLE	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area 29427-32874 and at area 19945-33212. Region 70511-70536 is covered by a single subclone. Region 18678-18873 is a double stranded single subclone. Areas 69557-70761, 89836-90416, 96951-99009, 105316-105607, and 133052-133152 are covered by Monsanto only. The nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto and Arizona Genomics Institute sequencing data.		
COMMENT	Location/Qualifiers		
	1. 137327		
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source	/mol_type="Genomic DNA"		
	/db_xref="taxon:39947"		
	/chromosome="3"		
	/clone="OJ1041F02"		
	/note="(japonica cultivar-group)"		
gene	complement(638..9495)		
	/gene="OJ1041F02.1"		
	/note="unknown protein"		
CDS	complement(join(638..838,1141..1276,3132..3244,3326..3421,3513..3727,3812..3934,4024..4054,4157..4216,5088..5243,		

5322. .5411.5484. .5699.5808. .5942.6035. .6538.6622. .66377,  
7548. .7593.7679. .7815.8196. .8328.9221. .9495))  
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/product="unknown protein"  
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/db\_xref="GI:29893590"  
/translation="WAGLELLLTIOFLMPDNDARQAEQRLARDPOVVPALVHLL  
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OPIILCKODESSKRVRIALAKAVGSFLEYNDGDGVKIRFDPSPGSLINRSCILAN  
GEEDVASIAEPFIDELIESPAVLGDSRVSIYQSELEVCNDELEINRQAOIISM  
LYKPAEKLKHKYVITPILOWCCLLTETAEDEDSDLAADRAAEVITDMAILPH  
VPPVLEPASVSFRHINKRIRBAVTSICGVSSGECCKIKRLEDCKLVCYIAEKDOE  
QMVRAASFAFGQFAEHLQPELTISHYESVLCCILNALEDPSDEVKESYIALAFCDE  
GMENTIPLNEDICLRARATEVVGIVAMAQGRAMETILPFTLEIAISGVLDISRLEY  
THGFSNVAEILDEDFAOYLPHVPLAFSSCNLDGSAVDDIDDDASVNDGSGVSSDD  
TVDFSPARNISIMLTITADIITLITVATRAIPRAHADVEXKODILDTVMNVIYKTMEDD  
KEVAQCTSLADIVRDCGFAITEPYITRLDATILILRQSSCCQVESDSBEDGDDID  
HDEVLMDVSDILPAFAKVMGVSFDPITKLPDLSIMKPAKSPPPQDKTVVATLAEV  
AQGMKAPISAVYDKIMPLVILKEIASSEATNRRNAFCVGENCKKGGAAALXYGDIIH  
GLHRTFAPSEEPDPAVRDNAAGAILAMIVQPSIPLNIIPLVDVNIAAQVVVSPN  
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12372. .15503  
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join(1,2372. .12757,12858. .13025,13130. .13295,13716. .13826,  
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EESKFTPPHSDVDFPMKQCPAIVFHRLLKLPVQDAEAYMLAI CQNDITRLIASGKSG  
SCSFETPDORFMKIVTKKSEVYVILRMRSYYEHHQSTLLTFYVTHICIKQAGCP  
KIHRRFDDKSGSHGRITDKTERKIDETITLKDLDQVAFRIQRFYEELMIOIMDCT  
PLETGQIMDVSLILGVHPRNDVSATKIGISOHIAFPKSTGRKSPGEGSFCGLCPVE  
SECKRDLIDSKRFTIQGLGIMNPAQESSKIIDNFIPLNRHLFITPPSGSGCDVYL  
FGGIIIDLDYDITKYLEHAYKSPQVNPDPVYSADVPKLYSRFPQDFIRVFIKEQ"  
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19263. .19454  
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21819. .24660  
/gene="OJ1041F02.3"  
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join(21819. .22007,22096. .22206,23772. .23996,24523. .24660)  
/gene="OJ1041F02.3"  
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TNDGKGKIHIEDAGETNDPKDAVDSVTKOISGIAISBILVATSSDADNKSSES  
SAPDDDKIRALKKIRLAEOYQDPENLKFEQLEKMKKILGMEKEELKLLENKSSPA  
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21819. .24660  
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/note="unknown protein"  
complement(join(26563. .26772,27082. .27288,27430. .27537,  
27881. .27940,28051. .28126,28327. .28484,28616. .28678,  
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/gene="OJ1041F02.4"  
/codon\_start=1  
/product="unknown protein"  
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Best Local Similarity	85.7%	Pred. No. 1.8e-06		
Matches 60	Conservative 0	Mismatched 10	Indels 0	Gaps 0
Db	119439	CCTGGCATTCTGAAACCAAGAGTACCTACTCCCAACATCCATCTTATCATGCA	123	
Qy	124	CTTCATGCA	133	
Db	119439	CCTTCATGCA	119430	

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RESULT 10
AX224398          50 bp      DNA          linear      PAT 10-SEP-2001
LOCUS             AX224398
DEFINITION        Sequence 5 from Patent WO0160997.
ACCESSION         AX224398
VERSION           AX224398.1 GI:15554640
KEYWORDS
SOURCE
ORGANISM          Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS          Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
TITLE            Male tissue-preferred regulatory region and method of using same
JOURNAL          Patent: WO 0160997-A 5 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
SOURCE           1..50
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                  /mol_type="unassigned DNA"
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ORIGIN
Query_Match      31.8%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred.No. 3.7e-05;
Matches          50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
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1 CTGAACCAAGAGATCTCTCTCCAAACATTCATCTTACTGATGCAAC 50
DB
RESULT 11
AX224399          40 bp      DNA          linear      PAT 10-SEP-2001
LOCUS             AX224399
DEFINITION        Sequence 6 from Patent WO0160997.
ACCESSION         AX224399
VERSION           AX224399.1 GI:15554641
KEYWORDS
SOURCE
ORGANISM          Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS          Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
TITLE            Male tissue-preferred regulatory region and method of using same
JOURNAL          Patent: WO 0160997-A 6 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
SOURCE           1..40
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                  /mol_type="unassigned DNA"
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Query_Match      25.5%; Score 40; DB 6; Length 40;
Best Local Similarity 100.0%; Pred.No. 0.066;
Matches          40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
85 AGGATACCTTCTCCCAACATTCATCTTACTGATGCAAC 124
1 AGGATACCTTCTCCCAACATTCATCTTACTGATGCAAC 40
DB
RESULT 12
BX950854          171896 bp   DNA          linear      VRT 03-FEB-2005
LOCUS             BX950854
DEFINITION        Zebrafish DNA sequence from clone CH211-125M22, complete sequence.
ACCESSION         BX950854
VERSION           BX950854.12 GI:58190604
KEYWORDS
HTG.

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SOURCE           Danio rerio (zebrafish)
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
AUTHORS          Pelan, S.
TITLE            Direct Submission
JOURNAL          Submitted (03-FEB-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 25, 2005 this sequence version replaced gi:56368832.
COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Center city: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WormPeP; Information
on the WormPeP database can be found at
http://www.sanger.ac.uk/projects/C_elgans/wormpep
Zebrafish pUC subclones occasionally display inconsistency over the
length of mononucleotide A/T runs and conserved TA repeats. Where
this is found the longest good quality representation will be
submitted.
Repeat names beginning 'vr' were identified by the Recon repeat
discovery system (Zhifeng Bao and Sean Eddy, submitted), and those
beginning 'dir' were identified by Rick Waterman (Stephen Johnson
lab, WashU). For further information see
http://www.sanger.ac.uk/projects/D_rerio/fishmask.shtml
CH211-125M22 is from a CHORI-211 BAC library
VECTOR: PTABAC2.1.
FEATURES
SOURCE           Location/Qualifiers
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/db_xref="taxon:7965"
/clone="CH211-125M22"
/clone_lib="CHORI-211"
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Query_Match      22.2%; Score 34.8; DB 5; Length 171896;
Best Local Similarity 52.8%; Pred.No. 3.1;
Matches          75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY
15 TGGGATACATCAAGTCTGTTCAACGTTGCTGTTCCATGTCACAGGCTTGCTTT 74
158604 TGGGATGTCATCTTACCAAGCTGGGTGTAAACCAACCAAGCTTTAAAGT 158545
DB
75 CTGAACCAAGAGATCTCTCTCCAAACATTCATCTTACTGATGCAAC 124
158544 AAGTAACTTCACTTAAATATTCATTTAAATCTGAATCTCACTTTAA 158485
QY
135 ACACGACATATGTTCTCGAA 156
DB
158484 ACTCCCATTTCTCATTTAA 158463

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RESULT 13  
AC104134 110127 bp DNA linear PRI 30-APR-2005  
DEFINITION Homo sapiens BAC clone RP11-525L16 from 2, complete sequence.  
AC104134  
VERSION AC104134.4 GI:19551199  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 110127)  
TITLE Doebber, A., Haakenson, W. and Tomlinson, C.  
JOURNAL The sequence of Homo sapiens BAC clone RP11-525L16  
REFERENCE 2 (bases 1 to 110127)  
AUTHORS Waterston, R.H.  
JOURNAL Direct Submission  
Submitted (04-DEC-2001) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE 3 (bases 1 to 110127)  
AUTHORS Waterston, R.H.  
JOURNAL Direct Submission  
Submitted (15-FEB-2002) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE 4 (bases 1 to 110127)  
AUTHORS Waterston, R.  
JOURNAL Direct Submission  
Submitted (15-FEB-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
REFERENCE 5 (bases 1 to 110127)  
AUTHORS Wilson, R.K.  
JOURNAL Direct Submission  
Submitted (30-APR-2005) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
COMMENT On Mar 20, 2002 this sequence version replaced gi:18677630.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu  
Contact: submissions@wustl.wustl.edu  
----- Summary Statistics  
Center project name: H\_NH0525L16  
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NOTICE:  
This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.  
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MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. Wes Warren,  
Department of Genetics, Washington University, St. Louis MO. For  
additional information about the map position of this sequence, see  
http://genome.wustl.edu  
-----  
SOURCE INFORMATION:  
The RP11-11 human BAC library was made from the blood of one male  
donor, as described by Osogawa, K., Moon, P. Y., Zhao, B., Frengen, E.,  
Tateno, M., Catanesi, J. J., and de Jong, P. J. (1998) An improved  
approach for construction of bacterial artificial chromosome  
libraries. Genomics 51:1-8. The clone may be obtained either from  
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong

and coworkers at http://www.chori.org  
VECTOR: pBACe3.6  
-----  
NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-554H10, 2000 bp overlap;  
the clone sequenced to the right is RP11-450E9, 2000 bp overlap.  
Actual start of this clone is at base position 151996 of  
RP11-554H10.  
-----  
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1. 110127  
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/chromosome="2"  
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34638..39571  
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/gene="FLJ25369"  
join(35632..35658,36392..36484,39039..39461)  
/gene="FLJ25369"  
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(FLJ25369), mRNA.; H\_NH0525L16.1  
This gene was based on gi(122749356)"  
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CHVKKVPIILNRKQPLMPFYQ"  
44296..44562  
/note="CpG island (GC=62.5, o/e=0.89, #CpGs=24)"  
59905..60161  
/note="CpG island (GC=66.5, o/e=0.76, #CpGs=22)"  
complement(66728..105650)  
/gene="EIF2AK3"  
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80861..81028,84653..85433,86541..86690,89505..89627,  
93417..93529,95828..96048,97969..98091,98748..98888,  
100430..100592,100805..101039,103259..103392,  
105456..105650))  
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93417..93529,95828..96048,97969..98091,98748..98888,  
100430..100592,100805..101039,103259..103392,  
105456..105650))  
/note="Homo sapiens eukaryotic translation initiation  
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DIVTKSVADMKVMAFSGKGGHLEMEYQFTPTPASMLLDQKYIPISLDDTSYTN  
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IILPPTIKMRPLHSPTPTLVLSGSDPCLSNDRFSHSEYSGALSIQPYDNY  
VLPPYKRNKRSQIIVRLPNDPVYKRNKQDPVLLHMKKEIVATILFICITATF  
IVRLFLPHDHPKKESETOCOTENKYNISGEANDSNMDKNSGYISRLDVEPI  
OCLEGRGFVGVPAKKNVDDCNALIKRIIRLPNELIAEKYMRVYKALAKIENQIVY  
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repeat_region      complement(29771..30036)
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repeat_region      32586..32654
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Query Match 21.9%; Score 34.4; DB 8; Length 214946;  
 Best Local Similarity 54.8%; Pred. No. 4.2; 56; Indels 0; Gaps 0;  
 Matches 68; Conservative 0; Mismatches 56

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QY      5 TCATCTCAGTCAGTACTGATCTGTTGAAACCGTTCCTGTTGCTTCCATGCAAGC 64
D      35745 TCATCTCTATGGGAGAGAAAATCATTTGACAAATATGACCATTTCCATGATGTAAC 35804
QY      65 CTGGCTTATCTGAAACCAAGAGATACCTGCTCCAAACATCCATCTTCTCATGCAAC 124
D      35805 ATCCACATACTAAGAAAGAGAGTAGCTTTTAACCCAAATAAATGTAACCTATGAAA 35864
QY      125 TTCC 128
D      35865 ATCC 35868

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## RESULT 15

```

CR847532      141554 bp      DNA      linear      HTG 15-JAN-2005
LOCUS      CR847532
DEFINITION      Danio rerio clone DKEYP-86C9, WORKING DRAFT SEQUENCE, 3 unordered
pieces.
ACCESSION      CR847532
VERSION      CR847532.4 GI:57863691
KEYWORDS      HTG; HTGS PHASE1; HTGS ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 141554)
REFERENCE
AUTHORS      Pelan,S.
TITLE      Direct Submission
JOURNAL      Submitted (14-JAN-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
On Jan 15, 2005 this sequence version replaced gi:56309949.
COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zkp86C9
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 141058 bases at least Q40
Consensus quality: 141224 bases at least Q30
Consensus quality: 141289 bases at least Q20
Insert size: 141354; sum-of-contigs
Insert size: 152619; 10.9% error; agarose-fp
Quality coverage: 8.68x in Q20 bases; sum-of-contigs Quality
coverage: 8.12x in Q20 bases; agarose-fp

```

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

FEATURES  
\* 1 10378: contig of 10378 bp in length  
\* 10379 10478: gap of 100 bp  
\* 10479 42327: contig of 31849 bp in length  
\* 42328 42427: gap of 100 bp  
\* 42428 141554: contig of 99127 bp in length.  
Location/Qualifiers  
1. 141554  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone\_id="DKXP-86C9"  
misc\_feature 1. 10378  
/note="assembly\_fragment:00017"  
misc\_feature 10479. 42327  
/note="assembly\_fragment:00290"  
misc\_feature 42428. 141554  
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ORIGIN  
Query Match 21.5%; Score 33.8; DB 14; Length 141554;  
Best Local Similarity 52.5%; Pred. No. 6.6;  
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 12 ACATGCACTACTACATGCTGTTCACCGTGTCTTGTTCATGCTCCAGCCTTGCT 71  
DB 90222 ACAGTGACCCCTACATCCTGTGTCTCATGATATGTACAGTGACAGGTTGGCT 90281  
QY 72 ATTCTGAACCAAGAGATACCTACCTCCAAACATCATCTTACTCATGCACTTCATG 131  
DB 90282 AAGTGGGAAATGGGATCATGTGCTCTGAAAAATGAAATTAATCAACAAAGAACTT 90341  
QY 132 CAAACGCGACATATGTTCC 152  
DB 90342 TCATAAACTTATTAGTCC 90362

Search completed: March 5, 2006, 21:55:45  
Job time : 687.29 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:08:23 ; Search time 104.48 Seconds (without adjustments)

10014.946 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1155\_1311  
Page: 157

Sequence: 1 cgtgtcatctcacatgcat.....cgacatatgtttcctgaac 157

Scoring table: IDENTITY\_NUC  
Ganon 10.0 Ganex 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Minimum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_21:★

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1: N_Geneseq1_21:*
2:   geneseq1_1980s:*
3:   geneseq1_1998s:*
4:   geneseq1_2000s:*
5:   geneseq1_2001as:*
6:   geneseq1_2001bs:*
7:   geneseq1_2002as:*
8:   geneseq1_2002bs:*
9:   geneseq1_2003as:*
10:  geneseq1_2003bs:*
11:  geneseq1_2003cs:*
12:  geneseq1_2003ds:*
13:  geneseq1_2004as:*
14:  geneseq1_2004bs:*
15:  geneseq1_2005as:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	157	100.0	255	5	AAH76340	Aah76340 Z. mays M
2	157	100.0	1394	2	AAK07408	Aak07408 Zea mays
3	157	100.0	1394	2	AAK07409	Aak07409 Zea mays
4	157	100.0	1394	5	AAH76332	Aah76332 Z. mays M
5	157	100.0	1394	5	AAH76333	Aah76333 Z. mays M
6	146	93.4	158	5	AAH76334	Aah76334 Z. mays M
7	54	34.0	2000	11	ACL8730	ACL8730 Rice str3
8	50	31.8	50	5	AAH76337	Aah76336 Z. mays M
9	40	25.5	40	5	AAH76337	Aah76337 Z. mays M
10	32.4	20.6	3267	12	ADKS211	Adks2131 Mouse alt1
11	31.6	20.1	2352	8	AAK48402	Aka48402 Prokaryote
12	31.4	20.0	15734	6	ABNH80329	Abnh80328 Human chr1
13	30.6	19.5	64415	3	AAK22279	Aak22279 BAC contig
14	30.6	19.5	79467	9	ADH02711	Adh02711 Mouse N18
15	30.6	19.5	79467	10	ADH72455	Adh72455 Mouse N18
16	30.6	19.5	79467	10	ADBS9565	Adbs9565 Mouse N18
17	30.4	19.4	52001	12	ADBE7076	Adbe7076 Human chr1
18	30.2	19.2	669	3	AAAS1436	Aaas1436 A. thaliana
19	30.2	19.2	1266	9	ADBS0983	Adbs0983 Allotococci

20	30	19.2	110000	5	AAB12064_07
21	30	19.1	30	9	AAH76335
22	30	19.1	378	10	ADD33403
23	30	19.1	396	10	ADD33403
24	29.8	19.0	373	4	AAH13328
25	29.8	18.9	1185	10	ADFO07936
26	29.6	18.7	110000	3	AAE22303_-2
27	29.2	18.6	1475	9	AAI62902
28	29.2	18.6	110000	2	AAI42053_-06
29	28.8	18.3	1500	8	ADM62984
30	28.6	18.2	756	13	ADMS7359
31	28.6	18.2	778	4	AAAS32892
32	28.6	18.2	778	4	AAAS32893
33	28.6	18.2	1043	10	ADD71973
34	28.6	18.2	1522	13	ADW62566
35	28.6	18.2	2160	6	ABN67847
36	28.6	18.2	2160	6	ABN67847
37	28.6	18.2	3231	13	ADAX1559
38	28.6	18.2	5115	11	ACNA4162
39	28.6	18.2	110000	8	ADD33806_-5
40	28.6	18.2	164702	3	ACF62730
41	28.6	18.2	164702	8	ADD20845
42	28.6	18.2	164702	10	ADB87934
43	28.6	18.2	164702	10	ADBB9517
44	28.6	18.2	164702	10	ADBB9517
45	28.6	18.1	1478	3	AAH15643
					AAH15643 Human pro
					Continuation (8 of
					AAH76335 Z. mays M
					Add33403 Mouse mit
					Add33404 Mouse mit
					Add33404 Mouse mit
					AAH13328 Human CDN
					ADFO07936 Bacterial
					Continuation (3 of
					AAI62902 Vermonta
					Continuation (7 of
					Ad662828 Arabidops
					Ad657319 Bacterial
					AAAS32892 Human gen
					AAAS32893 Human gen
					AAAS32893 Human ur
					ADW71973 Glycine n
					ADW65566 Glycine n
					ABN67847 Streptoco
					ABN67847 Streptoco
					ADAX1559 Plant fu
					ADAX1304 Plant fu
					ACNA4162 Human ge
					Continuation (6 of
					ACF62730.Cancer b
					Add20845 MRP1 base
					ADB87934 Human UG
					ADBB9517 Human MD
					ADBB9517 Human MD
					AAH15643 Human pro

## ALIGNMENTS

RESULT 1  
AAH76340  
ID AAH76340 standard; DNA; 255 BP.

DT 29-OCT-2001 (first entry)

DE Z. mays MS45 promoter fragment.

MS45; male tissue; regulatory region; transcription; male fertility;  
KW

XX  
XX  
XX

XX  
XX

XX  
XX

MOZ0016099 / -  
PN XX  
XX

PD 23-AUG-2001.  
XX

13-FEB-2001; 2001WC-US00452/

PR 15-FEB-2000; 2000US-00504487.  
XX

PA (PION-) PIONEER HI-BRED INT. INC.  
XX

PI Albertsen MC, Fox TW, Garnaat CW, Hultman G, Kendall TL,  
 YX

DR WPI: 2001-514772/56.  
XY

A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for

PT mediating fertility in a male plant.

PS Example 5; Fig 8; 50pp; English

CC The invention provides a male tissue-preferred regulatory region (I)

the MS45 gene. A method of mediating male fertility in a plant is

CC promoter operably linked to (I) into a plant where the exogenous gene

exogenous gene. A method of producing hybrid seeds is also provided. The

CC present sequence represents a Z. mays Ms45 promoter fragment  
XX  
SQ Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;  
Query Match 100.0%; Score 157; DB 5; Length 255;  
Best Local Similarity 100.0%; Pred. No. 1,4e-42;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTGTCACTTCACATGGCATCTACTACATGCTTGTCAACCGTTCGTTGTCATGCTCC 60  
DB 15 CGTGTCACTTCACATGGCATCTACTACATGCTTGTCAACCGTTCGTTGTCATGCTCC 74  
QY 61 AAGCTTGCCCTATTCTGAACCAAGAGATACCTACTCCCAACAATCATCTTACTCATG 120  
DB 75 AAGCTTGCCCTATTCTGAACCAAGAGATACCTACTCCCAACAATCATCTTACTCATG 134  
QY 121 CAACCTTCATGCAAAACGACGACATATGTTTCTTGAAAC 157  
DB 135 CAACCTTCATGCAAAACGACGACATATGTTTCTTGAAAC 171  
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ID AAK07408 standard; DNA; 1394 BP.  
XX  
AC AAK07408;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE Zea mays Ms45 male tissue-preferred regulatory region.  
XX  
KM Ms45; male; tissue-preferred; regulatory region; plant cells;  
XX plant tissue; differentiated; maize; hybrid seed; fertility; ss.  
XX  
OS Zea mays.  
XX  
PN MO9859061-A1.  
XX  
PD 30-DEC-1998.  
XX  
PF 19-JUN-1998; 98WO-US012895.  
XX  
PR 23-JUN-1997; 97US-00880499.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL,  
XX  
DR WPI; 1999-105628/09.  
XX  
PT New nucleic acid encoding a Ms45 male tissue-preferred regulatory region  
XX - useful in mediating plant fertility, especially hybrid seed production.  
XX  
PS Claim 2; Page 22-23; 39pp; English.  
XX  
CC The sequence is that encoding an Ms45 male tissue-preferred regulatory  
CC region. It may be used in the construction of a vector for a method of  
CC producing exogenous genes in a male tissue- preferred manner, which is  
CC useful in restoring or conferring fertility, such as in hybrid seed  
CC production. In conferring fertility, a monocot/dicot plant is transformed  
CC with the exogenous nucleotide sequence (a male sterility gene, preferably  
CC Ms45), which encodes a product selected from auxins, rolB and diptheria  
CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile  
CC and infertile plants  
XX  
SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;  
Query Match 100.0%; Score 157; DB 2; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 2,4e-42;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTGTCACTTCACATGGCATCTACTACATGCTTGTCAACCGTTCGTTGTCATGCTCC 60  
DB 15 CGTGTCACTTCACATGGCATCTACTACATGCTTGTCAACCGTTCGTTGTCATGCTCC 74

DB 1155 CGTGTCACTTCACATGGCATCTACTACATGCTTGTCAACCGTTCGTTGTCATGCTCC 1214  
QY 61 AAGCTTGCCCTATTCTGAACCAAGAGATACCTACTCCCAACAATCATCTTACTCATG 120  
DB 1215 AAGCTTGCCCTATTCTGAACCAAGAGATACCTACTCCCAACAATCATCTTACTCATG 1274  
QY 121 CAACCTTCATGCAAAACGACGACATATGTTTCTTGAAAC 157  
DB 1275 CAACCTTCATGCAAAACGACGACATATGTTTCTTGAAAC 1311  
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ID AAK07409 standard; DNA; 1394 BP.  
XX  
AC AAK07409;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE Zea mays Ms45 male tissue-preferred regulatory region.  
XX  
KM Ms45; male; tissue-preferred; regulatory region; plant cells;  
XX plant tissue; differentiated; hybrid seed; fertility; ss.  
XX  
OS Zea mays.  
XX  
PN MO9859061-A1.  
XX  
PD 30-DEC-1998.  
XX  
PF 19-JUN-1998; 98WO-US012895.  
XX  
PR 23-JUN-1997; 97US-00880499.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL,  
XX  
DR WPI; 1999-105628/09.  
XX  
PT New nucleic acid encoding a Ms45 male tissue-preferred regulatory region  
XX - useful in mediating plant fertility, especially hybrid seed production.  
XX  
PS Claim 3; Page 23-24; 39pp; English.  
XX  
CC The sequence is that encoding an Ms45 male tissue-preferred regulatory  
CC region. It may be used in the construction of a vector for a method of  
CC producing exogenous genes in a male tissue- preferred manner, which is  
CC useful in restoring or conferring fertility, such as in hybrid seed  
CC production. In conferring fertility, a monocot/dicot plant is transformed  
CC with the exogenous nucleotide sequence (a male sterility gene, preferably  
CC Ms45), which encodes a product selected from auxins, rolB and diptheria  
CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile  
CC and infertile plants  
XX  
SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;  
Query Match 100.0%; Score 157; DB 2; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 2,4e-42;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTGTCACTTCACATGGCATCTACTACATGCTTGTCAACCGTTCGTTGTCATGCTCC 60  
DB 1155 CGTGTCACTTCACATGGCATCTACTACATGCTTGTCAACCGTTCGTTGTCATGCTCC 1214  
QY 61 AAGCTTGCCCTATTCTGAACCAAGAGATACCTACTCCCAACAATCATCTTACTCATG 120  
DB 1215 AAGCTTGCCCTATTCTGAACCAAGAGATACCTACTCCCAACAATCATCTTACTCATG 1274  
QY 121 CAACCTTCATGCAAAACGACGACATATGTTTCTTGAAAC 157  
DB 1275 CAACCTTCATGCAAAACGACGACATATGTTTCTTGAAAC 1311

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RESULT 4
AAH76332
ID AAH76332 standard; DNA; 1394 BP.
XX
XX
AC AAH76332;
XX
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
XX
XX Ms45; male tissue; regulatory region; transcription; male fertility;
XX hybrid seed; ds.
XX
XX Zea mays.
XX
XX WO200160997-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 13-FEB-2001; 2001WO-US004527.
XX
XX PR 15-FEB-2000; 2000US-00504487.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Albertsen MC, Fox TW, Garnaat CM, Huffman G, Kendall TL;
XX
XX DR WPI; 2001-514772/56.
XX
XX PT A male tissue-preferred regulatory region comprising nucleotide sequences
XX essential for initiating transcription of the Ms45 gene useful for
XX mediating fertility in a male plant.
XX
XX PS Claim 4; Page 46; 50pp; English.
XX
XX CC The invention provides a male tissue-preferred regulatory region (I)
XX comprising nucleotide sequences essential for initiating transcription of
XX the Ms45 gene. A method of mediating male fertility in a plant is
XX provided that involves introducing an expression vector comprising a
XX promoter operably linked to (I) into a plant where the exogenous gene
XX impacts male fertility of the plant and (II) controls expression of the
XX exogenous gene. A method of producing hybrid seeds is also provided. The
XX present sequence represents a nucleic acid sequence encoding an Ms45 male
XX -tissue preferred regulatory region from Z. mays
XX
XX SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 157; DB 5; Length 1394;
XX Best Local Similarity 100.0%; Pred. No. 2,4e-42;
XX Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGGTGCATCTCAACAGGATACCTTCTTCAACCGTTCGTTGTCATGTC 60
XX DB 1155 CGGTGCATCTCAACAGGATACCTTCTTCAACCGTTCGTTGTCATGTC 1214
XX
XX QY 61 AGCCTTGCTTATTTGAAACCAAGGATACCTTCTTCAACCAATTCATCTTACTCANG 120
XX DB 1215 AGCCTTGCTTATTTGAAACCAAGGATACCTTCTTCAACCAATTCATCTTACTCANG 1274
XX
XX QY 121 CAACTTCATGCAAAACAGCAACATATGTTCTGTGAC 157
XX DB 1275 CAACTTCATGCAAAACAGCAACATATGTTCTGTGAC 1311
XX
XX RESULT 5
XX AAH76333
XX ID AAH76333 standard; DNA; 1394 BP.
XX
XX AC AAH76333;
XX
XX DT 29-OCT-2001 (first entry)
XX

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DE Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
XX
XX Ms45; male tissue; regulatory region; transcription; male fertility;
XX hybrid seed; ds.
XX
XX Zea mays.
XX
XX WO200160997-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 13-FEB-2001; 2001WO-US004527.
XX
XX PR 15-FEB-2000; 2000US-00504487.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Albertsen MC, Fox TW, Garnaat CM, Huffman G, Kendall TL;
XX
XX DR WPI; 2001-514772/56.
XX
XX PT A male tissue-preferred regulatory region comprising nucleotide sequences
XX essential for initiating transcription of the Ms45 gene useful for
XX mediating fertility in a male plant.
XX
XX PS Claim 4; Page 47; 50pp; English.
XX
XX CC The invention provides a male tissue-preferred regulatory region (I)
XX comprising nucleotide sequences essential for initiating transcription of
XX the Ms45 gene. A method of mediating male fertility in a plant is
XX provided that involves introducing an expression vector comprising a
XX promoter operably linked to (I) into a plant where the exogenous gene
XX impacts male fertility of the plant and (II) controls expression of the
XX exogenous gene. A method of producing hybrid seeds is also provided. The
XX present sequence represents a nucleic acid sequence encoding an Ms45 male
XX -tissue preferred regulatory region from Z. mays
XX
XX SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 157; DB 5; Length 1394;
XX Best Local Similarity 100.0%; Pred. No. 2,4e-42;
XX Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGGTGCATCTCAACAGGATACCTTCTTCAACCGTTCGTTGTCATGTC 60
XX DB 1155 CGGTGCATCTCAACAGGATACCTTCTTCAACCGTTCGTTGTCATGTC 1214
XX
XX QY 61 AGCCTTGCTTATTTGAAACCAAGGATACCTTCTTCAACCAATTCATCTTACTCANG 120
XX DB 1215 AGCCTTGCTTATTTGAAACCAAGGATACCTTCTTCAACCAATTCATCTTACTCANG 1274
XX
XX QY 121 CAACTTCATGCAAAACAGCAACATATGTTCTGTGAC 157
XX DB 1275 CAACTTCATGCAAAACAGCAACATATGTTCTGTGAC 1311
XX
XX RESULT 6
XX AAH76334
XX ID AAH76334 standard; DNA; 158 BP.
XX
XX AC AAH76334;
XX
XX DT 29-OCT-2001 (first entry)
XX
XX DE Z. mays Ms45 male tissue-preferred regulatory region fragment.
XX
XX Ms45; male tissue; regulatory region; transcription; male fertility;
XX hybrid seed; ds.
XX
XX Zea mays.
XX
XX WO200160997-A2.
XX

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PD 23-AUG-2001.  
XX  
PF 13-FEB-2001; 2001MO-US004527.  
XX  
PR 15-FEB-2000; 2000US-00504487.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Albersen MC, Fox TW, Garnaat CM, Huffman G, Kendall TL;  
XX WPI; 2001-514772/56.  
XX  
PT A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the Ms45 gene useful for  
PT mediating fertility in a male plant.  
XX  
PS Claim 5; Page 47; 50pp; English.  
XX  
CC The invention provides a male tissue-preferred regulatory region (I)  
CC comprising nucleotide sequences essential for initiating transcription of  
CC the Ms45 gene. A method of mediating male fertility in a plant is  
CC provided that involves introducing an expression vector comprising a  
CC promoter operably linked to (I) into a plant where the exogenous gene  
CC impacts male fertility of the plant and (I) controls expression of the  
CC exogenous gene. A method of producing hybrid seeds is also provided. The  
CC present sequence represents a DNA fragment -38 to -195 bases upstream of  
CC the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region  
CC nucleotide sequence  
XX  
SQ Sequence 158 BP; 41 A; 50 C; 21 G; 46 T; 0 U; 0 Other;  
XX  
Query Match 93.0%; Score 146; DB 5; Length 158;  
Best Local Similarity 99.4%; Pred. No. 6.1e-39;  
Matches 157; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
XX  
QY 1 CGGTGTCATCTGACATGCGATCTAGTCTGTTCAACCGTTGTC-TTGTTCATGCTC 59  
DB 1 CGGTGTCATCTGACATGCGATCTAGTCTGTTCAACCGTTGTTGTTTCATGCTC 60  
XX  
QY 60 CAAGCCTTGCTATTTCTGAACCAAGAGATACCTACTCTCCAAACAAATCCATCTTACAT 119  
DB 61 CAAGCCTTGCTATTTCTGAACCAAGAGATACCTACTCTCCAAACAAATCCATCTTACAT 120  
XX  
QY 120 GCAACTTCATGCAACAACGACATATGTTTCTCTGAAC 157  
DB 121 GCAACTTCATGCAACAACGACATATGTTTCTCTGAAC 158  
XX  
RESULT 7  
ACL38730  
ID ACL38730 standard; cDNA; 2000 BP.  
XX  
AC ACL38730;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE Rice stress-regulated promoter SEQ ID NO:17293.  
XX  
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;  
XX agriculture.  
XX  
OS Oryza sativa.  
XX  
PN WO2003008540-A2.  
XX  
PD 30-JAN-2003.  
XX  
PF 21-JUN-2002; 2002MO-US019668.  
XX  
PR 22-JUN-2001; 2001US-0300112P.  
XX 24-AUG-2001; 2001US-0314662P.  
XX 26-SEP-2001; 2001US-0325277P.  
XX 21-NOV-2001; 2001US-0332132P.  
XX

XX  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Karagiri F;  
XX Moughamer T, Provart N, Rieke D, Zhu T;  
XX WPI; 2003-248011/24.  
XX  
PT New stress-responsive nucleic acid, useful for altering the  
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
PT stress, salt stress or osmotic stress.  
XX  
PS Claim 48; SEQ ID NO 17293; 89pp; English.  
XX  
CC The invention relates to novel abiotic stress responsive polynucleotides  
CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
CC cells, and plants containing such polynucleotides. Also disclosed are  
CC methods for using the polynucleotides and polypeptides to alter the  
CC responsiveness of a plant to abiotic stress. The invention is useful in  
CC agriculture. The nucleic acid is useful for determining whether a test  
CC plant has been exposed to an abiotic stress condition. It is also useful  
CC for selecting an agent that alters abiotic stress regulated  
CC polynucleotide expression in a plant cell, and to identify a homolog or  
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
CC molecule and the polypeptide encoded by it are useful in altering the  
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
CC stress, osmotic stress or any of their combinations. The present sequence  
CC is used in the exemplification of the invention  
XX  
SQ Sequence 2000 BP; 616 A; 370 C; 355 G; 659 T; 0 U; 0 Other;  
XX  
Query Match 34.4%; Score 54; DB 11; Length 2000;  
Best Local Similarity 85.7%; Pred. No. 1.2e-07;  
Matches 60; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
XX  
QY 64 CTTTGCTATTTCGAACCAAGAGATACCTACTCTCCAAACAAATCCATCTTACTGACAA 123  
DB 1819 CTTTGCTATTTCGAACCAAGAGATACCTACTCTCCAAACAAATCCATCTTACTGACAA 1878  
XX  
QY 124 CTTTCATGCA 133  
DB 1879 CTTTCATGCA 1888  
XX  
RESULT 8  
AAH76336  
ID AAH76336 standard; DNA; 50 BP.  
XX  
AC AAH76336;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Z. mays Ms45 male tissue-preferred regulatory region fragment.  
XX  
KW Ms45; male tissue; regulatory region; transcription; male fertility;  
XX hybrid seed; ds.  
XX  
OS Zea mays.  
XX  
PN WO200160997-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 13-FEB-2001; 2001MO-US004527.  
XX  
PR 15-FEB-2000; 2000US-00504487.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Albersen MC, Fox TW, Garnaat CM, Huffman G, Kendall TL;  
XX WPI; 2001-514772/56.  
XX  
DR

PT A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the MS45 gene useful for  
XX mediating fertility in a male plant.  
XX  
PS Claim 5; Page 47; 50pp; English.  
XX  
CC The invention provides a male tissue-preferred regulatory region (I)  
CC comprising nucleotide sequences essential for initiating transcription of  
CC the MS45 gene. A method of mediating male fertility in a plant is  
CC provided that involves introducing an expression vector comprising a  
CC promoter operably linked to (i) into a plant where the exogenous gene  
CC impacts male fertility of the plant and (ii) controls expression of the  
CC exogenous gene. A method of producing hybrid seeds is also provided. The  
CC present sequence represents a DNA fragment -72 to -111 bases upstream of  
CC the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region  
XX nucleotide sequence  
XX  
SQ Sequence 50 BP; 18 A; 17 C; 5 G; 10 T; 0 U; 0 Other;  
XX  
Query Match 31.8%; Score 50; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 75 CTGAACCAAGAGATCTACTCTCCCAACATCCATCTTACTGCAAC 124  
1 CTGAACCAAGAGATCTACTCTCCCAACATCCATCTTACTGCAAC 50  
XX  
RESULT 9  
AAH76337  
ID AAH76337 standard; DNA; 40 BP.  
XX  
AC AAH76337;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Z. mays Ms45 male tissue-preferred regulatory region fragment.  
XX  
KM Ms45; male tissue; regulatory region; transcription; male fertility;  
XX hybrid seed; ds.  
XX  
OS Zea mays.  
XX  
PN WO200160997-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 13-FEB-2001; 2001WO-US004527.  
XX  
PR 15-FEB-2000; 2000US-00504487.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Albrechtsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL,  
XX WPI; 2001-514772/56.  
XX  
DR A male tissue-preferred regulatory region comprising nucleotide sequences  
XX essential for initiating transcription of the MS45 gene useful for  
XX mediating fertility in a male plant.  
XX  
PS Claim 14; Page 32; 50pp; English.  
XX  
CC The invention provides a male tissue-preferred regulatory region (I)  
CC comprising nucleotide sequences essential for initiating transcription of  
CC the MS45 gene. A method of mediating male fertility in a plant is  
CC provided that involves introducing an expression vector comprising a  
CC promoter operably linked to (i) into a plant where the exogenous gene  
CC impacts male fertility of the plant and (ii) controls expression of the  
CC exogenous gene. A method of producing hybrid seeds is also provided. The  
CC present sequence represents a DNA fragment upstream of the TATA box of a  
CC Z. mays Ms45 male-tissue preferred regulatory region nucleotide sequence  
XX

SQ Sequence 40 BP; 14 A; 14 C; 3 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 25.5%; Score 40; DB 5; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 85 AGATATCTTACTCTCCCAACATCCATCTTACTGCAAC 124  
1 AGATATCTTACTCTCCCAACATCCATCTTACTGCAAC 40  
XX  
RESULT 10  
ADK52131  
ID ADK52131 standard; cDNA; 3267 BP.  
XX  
AC ADK52131;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Mouse atopic-dermatitis/psoriasis-associated EST #4.  
XX  
KM Mouse; 88; EST; atopic dermatitis; psoriasis; dermatological;  
XX anti-inflammatory; antipruritic; rash; expressed sequence tag.  
XX  
OS Mus musculus.  
XX  
PN WO2004016785-A1.  
XX  
PD 26-FEB-2004.  
XX  
PF 06-AUG-2003; 2003WO-JP009999.  
XX  
PR 06-AUG-2002; 2002JP-00229319.  
XX 14-MAY-2003; 2003JP-00136544.  
XX  
PA (GENO-) GENOX RES INC.  
XX (UTSU-) UNIV JUNTENDO.  
XX  
PI Itch M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C,  
XX Mitsush K;  
XX WPI; 2004-214514/20.  
XX  
DR Detecting atopic dermatitis or psoriasis comprises assaying levels of  
XX expression of an indicator gene at a rash site and non-rash site of a  
XX person with atopic dermatitis or psoriasis.  
XX  
PS Claim 20; SEQ ID NO 164; 484pp; Japanese.  
XX  
CC The invention relates to detecting atopic dermatitis or psoriasis  
CC comprising assaying the levels of expression of an indicator gene at a  
CC rash site and non-rash site of a person with atopic dermatitis or  
CC psoriasis comparing these levels with those of a healthy person, and  
CC determining that if the levels of indicators are higher or lower, then  
CC this indicates the disease. Also included are a reagent for detecting  
CC atopic dermatitis or psoriasis, a kit for screening for treatments, a  
CC transgenic non human vertebrate animal models for the diseases, an agent  
CC for inducing the diseases in mice and a DNA chip for assaying for the  
CC indicator genes. The method is used for treatment, detection and animal  
CC models for research of atopic dermatitis/ psoriasis-associated EST  
CC (expressed sequence tag).  
XX  
SQ Sequence 3267 BP; 1029 A; 658 C; 590 G; 990 T; 0 U; 0 Other;  
XX  
Query Match 20.6%; Score 32.4; DB 12; Length 3267;  
Best Local Similarity 54.1%; Pred. No. 2.5;  
Matches 66; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
XX  
QY 27 TGCCTTTTCAACCGTGTGCTTGTTCATCTCCCAAGCCTTCTGAAACCAAG 86  
2774 TGCCTTTTCAACCGTGTGCTTGTTCATCTCCCAAGCCTTCTGAAACCAAGT 2833  
XX

Qy 87 GATACCTACTCCCAACATCATCTTACTGATGCAATTCATGCAACGACGACATAT 146  
 Db 2834 GTTCTAGTTCCCAAGAGCATTTTGGCACTAGCGTCAACATCTAAGACCTGAAT 2893  
 Qy 147 GT 148  
 Db 2894 GT 2895  
 RESULT 11  
 ACA48402/c  
 ID ACA48402 standard; DNA; 2352 BP.  
 XX ACA48402;  
 XX 19-JUN-2003 (first entry)  
 XX DE Prokaryotic essential gene #30059.  
 XX KM Antisense; ds: prokaryotic essential gene; cell proliferation;  
 XX KM drug design; gene.  
 OS Streptococcus mutans.  
 XX MO20027183-A2.  
 XX PD 03-OCT-2002.  
 XX PF 21-MAR-2002; 2002WO-US009107.  
 XX PR 21-MAR-2001; 2001US-00815242.  
 XX PR 06-SEP-2001; 2001US-00948993.  
 XX PR 25-OCT-2001; 2001US-0342923P.  
 XX PR 08-FEB-2002; 2002US-00072851.  
 XX PR 06-MAR-2002; 2002US-0362699P.  
 XX PA (ELIT-) ELITRA PHARM INC.  
 PI Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 DR WPI; 2003-029926/02.  
 XX P-PSDB; ABU44532.  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 PS Claim 14; SEQ ID NO 36272; 1766bp; English.  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-regulated gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
 CC prokaryotic essential genes. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SO Sequence 2352 BP; 762 A; 401 C; 500 G; 689 T; 0 U; 0 Other;  
 Query Match 20.1%; Score 31.6; DB 8; Length 2352;  
 Best Local Similarity 58.5%; Pred. No. 4.2;  
 Matches 55; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
 Qy 62 AGCCTGCTATTCTGAAACGAGATACCTACTCCCAACATCATCTTACTGATGC 121  
 Db 234 ATCTGACTGTGCCCCAAGAGCATCTCTGAAAATCTGTCTACATCTGC 175  
 Qy 122 AACTTCATGCAACAGCACATATGTTTCTGA 155  
 Db 174 AATTTGCAAAAGAAAGTTCAATTTTCTCTGA 141  
 RESULT 12  
 ABN80329/c  
 ID ABN80329 standard; DNA; 15734 BP.  
 XX  
 AC ABN80329;  
 XX  
 XX 15-JUL-2002 (first entry)  
 XX DE Human chemically modified disease associated gene SEQ ID NO 346.  
 XX KM Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;  
 KM heart disease; epilepsy; histone deacetylation; muscular dystrophy;  
 KM dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;  
 KM antidiabetic; cytostatic; anticonvulsant; ds.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX MO200200927-A2.  
 XX PD 03-JAN-2002.  
 XX PF 02-JUL-2001; 2001WO-EP007536.  
 XX PR 30-JUN-2000; 2000DE-01032529.  
 XX PR 01-SEP-2000; 2000DE-01043826.  
 XX PA (EPIC-) EPIDENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 DR WPI; 2002-130908/17.  
 PT Novel nucleic acid useful for diagnosis and therapy of diseases  
 PT associated with development genes such as diabetes, comprises a sequence  
 PT of a segment of chemically pretreated DNA of genes associated with  
 PT development.  
 PS Claim 1; SEQ ID NO 346; 27bp; English.  
 CC The invention relates to a nucleic acid (I) comprising a sequence at  
 CC least 18 bases in length of a segment of chemically pretreated DNA (II)  
 CC of genes associated with development selected from 87 genes listed in the  
 CC specification such as ACPN, ADFN, or AFD1 and comprising one of 350  
 CC sequences (ABN79984-ABN80333) or their complements. The invention is  
 CC useful for the diagnosis or therapy of diseases associated with  
 CC development genes, in particular diseases related to homeobox containing  
 CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes  
 CC associated with congenital heart disease, epilepsy, diseases related to

CC histone deacetylation, Curarino syndrome, diseases related with the  
CC development of the brain and limb girdle muscular dystrophy and dwarfism.  
CC Oligomers specific to each of the genes are useful for detecting the  
CC methylation state of all CpG dinucleotides within the 350 sequences or  
CC (II) and their complementary sequences, as primer oligonucleotides for  
CC the amplification of the 350 sequences, (III) and/or their complements and  
CC as oligomer probes for detecting the cytosine methylation state and/or  
CC single nucleotide polymorphisms (SNPs). Note: The sequence data for this  
CC patent did not form part of the printed specification but is based on  
CC sequence information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 15734 BP; 3630 A; 744 C; 4234 G; 7126 T; 0 U; 0 Other;  
Query Match 20.0%; Score 31.4; DB 6; Length 15734;  
Best Local Similarity 59.6%; Pred. No. 9;  
Matches 53; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 52 CCATGCTCAAGCTTGGCTTATTTGACCAAGAGATCTTCCCAACATTCATC 111  
DB 8802 CCTCTCTTCTCCCTTATGATCTTAAACATCAAAACCTTAATTAACCAACCAAC 8743  
QY 112 TTACTGATGCACTTCATGCAACAGC 140  
DB 8742 TACTTAACCACTCTTCAATTAACACCC 8714  
RESULT 13  
ID AAF22279 standard; DNA; 64415 BP.  
XX AAF22279;  
AC AAF22279;  
XX  
DT 20-MAR-2001 (first entry)  
XX  
DE BAC containing repeats from centromeres 1-4 #2.  
XX  
KM Centromere; mitosome; vector; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO20005325-A2.  
XX  
PD 21-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-US007392.  
XX  
PR 18-MAR-1999; 99US-0125219P.  
XX  
PR 01-APR-1999; 99US-0127409P.  
XX  
PR 18-MAY-1999; 99US-0134770P.  
XX  
PR 13-SEP-1999; 99US-015384P.  
XX  
PR 17-SEP-1999; 99US-0154603P.  
XX  
PR 16-DEC-1999; 99US-0172493P.  
XX  
PA (UYCH-) UNIV CHICAGO.  
XX  
PI Preuss D, Copenhagen G, Keith K;  
XX  
DR WPI; 2000-587529/55.  
XX  
PT Recombinant DNA construct comprising a plant centromere, useful for  
XX producing stably inherited mitosomes which can serve as vectors for the  
XX construction of transgenic plant and animal cells.  
XX  
FS Claim 102; Page 321-335; 1449P; English.  
XX  
CC The present invention relates to a recombinant DNA construct of a plant  
XX (Arabidopsis thaliana) centromere. The constructs are useful for  
XX producing stably inherited mitosomes which can serve as vectors for the  
XX construction of transgenic plant and animal cells expressing selected  
XX proteins such as hormones, enzymes, interleukins, clotting factors,  
XX cytokines, antibodies, and growth factors  
XX  
SQ Sequence 64415 BP; 18698 A; 13554 C; 13083 G; 18980 T; 0 U; 100 Other;

Query Match 19.5%; Score 30.6; DB 3; Length 64415;  
Best Local Similarity 58.1%; Pred. No. 26;  
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
QY 65 CTGGCTTCTTCAACCAAGAGATCTTCACTCCCAACCAATCTTCAATCAAC 124  
DB 7117 CTGCTCTTTAGTATTTATGATATTTCTCTTCAACCACTTAACCTTCAACC 7176  
QY 125 TTCAATGCAACAGCAATATGTTCTGAAC 157  
DB 7177 TTAAATCCAAACCTTAATCTAATCTTCAAC 7209  
RESULT 14  
ID ADA02717 standard; DNA; 79467 BP.  
XX ADA02717;  
AC ADA02717;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Mouse NFatcl carcinoma associated gene, SEQ ID NO:1235.  
XX  
KM Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;  
XX prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;  
XX gene; ds.  
XX  
OS Mus sp.  
XX  
PN WO2003057146-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041414.  
XX  
PR 26-DEC-2001; 2001US-00035832.  
XX  
PA (SAGR-) SAGRES DISCOVERY.  
XX  
PI Morris DW;  
XX  
DR WPI; 2003-587068/55.  
XX  
PT New recombinant nucleic acid encoding carcinoma associated protein,  
XX useful for preparing compositions for treating carcinomas.  
XX  
PS Claim 1, SEQ ID NO 1235; 245P; English.  
XX  
CC The invention relates to recombinant carcinoma associated (CA) nucleic  
XX acid sequences from mouse and human (ADA01482-ADA03094), and to  
XX recombinant carcinoma associated proteins (CAP) encoded by them. The  
XX invention also encompasses expression vectors and host cells comprising a  
XX CA nucleic acid, a polypeptide (especially an antibody) that specifically  
XX binds to the protein, and a biochip comprising CA nucleic acid or  
XX oncogenic retroviruses, which insert into the genome of the host organism  
XX at random. Many of these do not carry transduced host oncogenes or  
XX pathogenic trans-acting viral genes, meaning that cancer incidence is a  
XX direct consequence of the effects of proviral integration into host  
XX protooncogenes. The CA nucleic acid sequences can be used to diagnose  
XX carcinoma (especially breast cancer, prostate cancer, lymphoma or  
XX leukaemia) or a propensity to carcinoma by determination of the sequence  
XX of a CA gene, or by determination of CA gene expression in particular  
XX tissues. CA nucleic acids, proteins and antibodies are also useful as  
XX therapeutic agents and in screening and evaluating drug candidates. The  
XX present sequence represents a specifically claimed murine CA nucleic acid  
XX patent did not form part of the printed specification, but was obtained  
XX in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pcr\_sequences.  
XX  
SQ Sequence 79467 BP; 18256 A; 19684 C; 20064 G; 20204 T; 0 U; 1261 Other;

Query Match 19.5%; Score 30.6; DB 9; Length 79467;  
Best Local Similarity 56.4%; Pred. No. 28;  
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Search completed: March 5, 2006, 18:11:42  
Job time : 105.48 secs

QY 51 TCCATCGTCCAGCCTTGCTTATTTGAAACCAAGATACCTACCTCCAAACAATCCAT 110  
DB 53779 TCCACTAATGATCTTCTCTCTGGAACAAGCTGAGTCTTAGTCACACACACACA 53838  
QY 111 CTTACTCATGCACTTCATGCAACGACATATGTTTC 151  
DB 53839 CACACACACACACACACACACACACACAGCTGTGGCTC 53879

## RESULT 15

ADB72455  
ID ADB72455 standard; DNA; 79467 BP.

AC ADB72455;

DT 04-DEC-2003 (first entry)

DE Mouse Nfatc1 gene.

XX mouse; ds; cytosstatic; gene therapy; vaccine; carcinoma; lymphomas;  
KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.

OS Mus BP.

PN W02003008583-A2.

XX 30-JAN-2003.

XX 26-DEC-2001; 2001WO-US051291.

XX 02-MAR-2001; 2001US-00798586.

XX 23-OCT-2001; 2001US-00004113.

XX 08-NOV-2001; 2001US-00052482.

XX 30-NOV-2001; 2001US-00997722.

XX 20-DEC-2001; 2001US-00034650.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW, Engelhard EK;

XX WPI; 2003-239337/23.

XX Claim 1; SEQ ID NO 283; 2304pp; English.

XX The invention relates to a novel recombinant nucleic acid comprising a

XX nucleotide sequence selected from any of the 660 sequences fully defined

XX in the specification. A polynucleotide of the invention has cytostatic

XX activity, and may have a use in gene therapy, or in a vaccine. The

XX recombinant nucleic acids and polypeptides are useful for treating

XX carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and

XX sarcomas. The present sequence represents a mouse gene of the invention.

XX Sequence 79467 BP; 18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;

QY Query Match 19.5%; Score 30.6; DB 10; Length 79467;

DB Best Local Similarity 56.4%; Pred. No. 28;

Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 51 TCCATCGTCCAGCCTTGCTTATTTGAAACCAAGATACCTACCTCCAAACAATCCAT 110

DB 53779 TCCACTAATGATCTTCTCTCTGGAACAAGCTGAGTCTTAGTCACACACACACA 53838

QY 111 CTTACTCATGCACTTCATGCAACGACATATGTTTC 151

DB 53839 CACACACACACACACACACACACACACAGCTGTGGCTC 53879

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 18:11:59; Search time 741.207 Seconds  
(without alignments)  
9910.279 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1155\_1311

Sequence: 1 cgtgtcatctccacatgacatgcacacacatgcttcctgaac 157

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 segs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_est4:  
5: gb\_est5:  
6: gb\_est6:  
7: gb\_est7:  
8: gb\_est8:  
9: gb\_est9:  
10: gb\_est10:  
11: gb\_est11:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	100.0	687	9	CC656939 OGMDO20TV
2	157	100.0	915	10	CG242425 OGIAG08TV
3	157	100.0	963	9	CC656933 OGMDO20TV
4	47	29.9	296	10	CM445575 fdbb001f1
5	47	29.9	296	10	CM445575 fdbb001f1
6	37.8	24.1	636	10	CE588104 tigr-gss-
7	37.8	24.1	643	7	CO669495
8	35.6	22.7	1085	10	AC366773 Mus muscu
9	35.6	22.7	874	10	C2727957 OC_Ba005
10	34	21.5	700	2	BR505306
11	33.8	21.5	734	10	CG871670 rhesu3c3-4
12	33.6	20.9	440	1	AL1744861 t16b06.x
13	32.8	20.8	648	8	CM446438 OGI_X2G22
14	32.6	20.8	740	10	CM558661 OA_ABA008
15	32.6	20.8	758	10	CM5597425
16	32.6	20.8	775	8	CM442481 OGI_X2G64
17	32.6	20.8	804	7	CM575123
18	32.6	20.8	843	10	CM599444 OA_ABA013
19	32.6	20.8	864	8	CM404228 OGI_X2T35
20	32.6	20.8	868	8	DN096073 OGI_CABE6
21	32.6	20.8	1101	10	DN096073 OGI_CABE6
22	32.6	20.8	1101	10	AL064557 Drosophila

23	32.4	20.6	347	2	BE690384
24	32.4	20.6	483	1	AJ746802
25	32.4	20.6	497	1	AW990724
26	32.4	20.6	498	2	BE632212
27	32.4	20.6	500	2	BF225639
28	32.4	20.6	527	2	BE448824
29	32.4	20.6	528	7	CM243061
30	32.4	20.6	539	5	BK528623
31	32.4	20.6	542	1	AA673664
32	32.4	20.6	543	2	BE133867
33	32.4	20.6	545	2	BF020472
34	32.4	20.6	547	5	BK517541
35	32.4	20.6	570	2	BE134144
36	32.4	20.6	621	1	BR004373
37	32.4	20.6	742	3	BT453933
38	32.4	20.6	859	10	CNS0004Y
39	32.4	20.6	919	2	BE682258
40	32.4	20.6	1039	11	CNS0531A
41	32.4	20.6	2194	4	BC048853
42	32.4	20.6	2454	4	AK028832
43	32.2	20.5	432	9	BH752563
44	32.2	20.5	960	10	DU054394
45	32.2	20.5	979	10	C2954687

ALIGNMENTS

RESULT 1  
LOCUS CC656939 687 bp DNA linear GSS 19-JUN-2003  
DEFINITION OGMDO20TV ZM 0.7 1.5 KB zea mays genomic clone ZMBM0554D15,  
genomic survey sequence.  
ACCESSION CC656939  
VERSION CC656939.1 GI:32060231  
KEYWORDS GSS.  
SOURCE zea mays  
ORGANISM zea mays  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 687)  
White, C.A., Frazer, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Renwick, A., Frazer, C.A., Budiman, M.A., Bedell, J.A., Konliff, T.,  
Citek, R.W., Nunez, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGMDO20TV  
Contact: Cathy Whitelaw

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
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/organism="Zea mays"  
/mol\_type="genomic DNA"  
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/clone="ZMBM0554D15"  
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methylation filtered genomic DNA library"

ORIGIN  
Query Match 100.0%; Score 157; DB 9; Length 687;  
Best Local Similarity 100.0%; Pred. No. 2.2e-35;  
Matches 157; Conservative 0; Mismatches 0; Gaps 0;

1 CGTGTCTCATCTACATGACATCTACATCTTGTCAACCGTGTCTTGTTCATCTCC

Db 421 CGTGTCACTCAGCATGGCATCTACATGCTGTTCACCGTTCCTGTTCCATCGCC 362  
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Qy 61 AAGCTTGCCATATTCGAACCAAGAGATACCTCTCCCAAAATCATCTTCTCATG 120  
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Db 361 AAGCTTGCCATATTCGAACCAAGAGATACCTCTCCCAAAATCATCTTCTCATG 302  
|||  
Qy 121 CAATTCATGCAAAACAGCATATGTTCTCTGAAC 157  
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Db 301 CAATTCATGCAAAACAGCATATGTTCTCTGAAC 265  
|||  
RESULT 2 915 bp DNA linear GSS 22-AUG-2003  
CG224225  
LOCUS OGIAG08TV\_ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMMBMA0716B15,  
DEFINITION genomic survey sequence.  
ACCESSION CG224225  
VERSION CG224225  
KEYWORDS GI:34124113  
SOURCE GSS.  
ORGANISM Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 915)  
Whitejaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGIAG08TV  
Contact: Cathy Whitejaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitejaw@tigr.org  
Seq primer: TR  
Class: methylation filtered.  
Location/Qualifiers  
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FEATURES  
source

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Query Match 100.0%; Score 157; DB 10; Length 915;  
Best Local Similarity 100.0%; Pred. No. 2.4e-39;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGTCACTCAGCATGGCATCTACATGCTGTTCACCGTTCCTGTTCCATCGCC 60  
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Db 534 CGTGTCACTCAGCATGGCATCTACATGCTGTTCACCGTTCCTGTTCCATCGCC 593  
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Qy 61 AAGCTTGCCATATTCGAACCAAGAGATACCTCTCCCAAAATCATCTTCTCATG 120  
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Db 594 AAGCTTGCCATATTCGAACCAAGAGATACCTCTCCCAAAATCATCTTCTCATG 653  
|||  
Qy 121 CAATTCATGCAAAACAGCATATGTTCTCTGAAC 157  
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Db 654 CAATTCATGCAAAACAGCATATGTTCTCTGAAC 690  
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RESULT 3 963 bp DNA linear GSS 19-JUN-2003  
CC656933  
LOCUS CG656933\_ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMMBMA0554D15,  
DEFINITION OGMDO20TV

ACCESSION genomic survey sequence.  
CC656933  
VERSION CG656933.1 GI:32060225  
KEYWORDS GSS.  
SOURCE Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 963)  
Whitejaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGMDO20TV  
Contact: Cathy Whitejaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitejaw@tigr.org  
Seq primer: TR  
Class: methylation filtered.  
Location/Qualifiers  
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/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

FEATURES  
source

ORIGIN

Query Match 100.0%; Score 157; DB 9; Length 963;  
Best Local Similarity 100.0%; Pred. No. 2.4e-39;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGTCACTCAGCATGGCATCTACATGCTGTTCACCGTTCCTGTTCCATCGCC 60  
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Db 752 CGTGTCACTCAGCATGGCATCTACATGCTGTTCACCGTTCCTGTTCCATCGCC 811  
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Qy 61 AAGCTTGCCATATTCGAACCAAGAGATACCTCTCCCAAAATCATCTTCTCATG 120  
|||  
Db 812 AAGCTTGCCATATTCGAACCAAGAGATACCTCTCCCAAAATCATCTTCTCATG 871  
|||  
Qy 121 CAATTCATGCAAAACAGCATATGTTCTCTGAAC 157  
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Db 872 CAATTCATGCAAAACAGCATATGTTCTCTGAAC 908  
|||  
RESULT 4 702 bp DNA linear GSS 31-OCT-2004  
CW324514  
LOCUS CW324514.1 GI:55040702  
DEFINITION 104 819 11477203 148 35910 078 Sorghum methylation filtered library  
(t4b1d:104) Sorghum bicolor genomic clone 11477203, genomic survey  
sequence.  
ACCESSION CW324514  
VERSION CW324514.1 GI:55040702  
KEYWORDS GSS.  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor

REFERENCE  
AUTHORS  
Jones,J., Flick,E., Budiman,M.A., Nurnberg,A., Citek,R.W., Robbins,D.,  
McKenamy,J., Smith,M., Holzman,H., Roe,B.A., Wiley,G., Korf,I.F.,  
Rabinowicz,P.D., Lakey,N., McComble,W.R., Jeddeloh,J.A. and  
Martensen,R.A.

TITLE Sorghum genome sequencing by methylation filtration  
JOURNAL PLOS Biol. 3 (1), e13 (2005)  
PUBMED 15660154  
COMMENT

CONTACT: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: 819 row: c column: 19  
Seq primer: SMFOR Forward  
Class: methylation filtered  
High quality sequence stop: 702.  
Location/Qualifiers  
1..702  
/organism="Sorghum bicolor"  
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/note="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN  
Query Match 40.1%; Score 63; DB 10; Length 702;  
Best Local Similarity 93.0%; Pred. No. 3.9e-09;  
Matches 66; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 64 CCTGGCTATTCGACCAAGAGATACCTCTCCCAACATCATCTTACATCGAA 123  
LOCUS  
DB 53 CCTGGCTATTCGACCAAGAGATACCTCTCCCAACATCATCTTACATCGAA 112

QY 124 CTTCCATCGCA 134  
DB 113 CTTCCATCGCA 123

RESULT 5 296 bp DNA linear GSS 02-NOV-2004  
CMA45575  
LOCUS fdb001f170ml6k0 Sorghum methylation filtered library (LibID: 104)  
DEFINITION Sorghum bicolor genomic clone fdb001f170ml6, genomic survey sequence.  
ACCESSION CMA45575  
VERSION CMA45575.1 GI:55193536  
KEYWORDS  
SOURCE  
ORGANISM Sorghum bicolor (Sorghum)  
GSS.  
Sorghum bicolor  
Sorghum bicolor  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 296)  
Bedell, J.A., Budiman, M.A., Numborg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, W., Holman, H., Koe, B.A., Wiley, G., Korf, I.F., Rabinowitz, P.D., Lakey, N., McCombe, W.R., Jeddelin, D.A. and Martienssen, R.A.  
Sorghum genome sequencing by methylation filtration  
PLOS Biol. 3 (1), e13 (2005)  
15660154  
CONTACT: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: fdb001f170 row: m column: 16

Seq primer: k Reverse  
Class: methylation filtered  
High quality sequence stop: 296.  
Location/Qualifiers  
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ORIGIN  
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Matches 64; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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DB 221 CCTGGCTATTCGACCAAGAGATACCTCTCCCAACATCCATCTTACTCATCGA 280

QY 123 ACTTCCATCGCA 137  
DB 281 ACTTCCATCGCA 295

RESULT 6 636 bp DNA linear GSS 28-SEP-2003  
CE588104/c  
LOCUS tigr-gss-dog-1700036359543 Dog Library Canis familiaris genomic, genomic survey sequence.  
DEFINITION  
ACCESSION CE588104  
VERSION CE588104.1 GI:36904885  
KEYWORDS  
SOURCE  
ORGANISM Canis familiaris (dog)  
GSS.  
Canis familiaris  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 636)  
Kirkness, E.F., Rafina, V., Halpern, A.L., Levy, S., Remington, K., Ruesch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
14512627  
CONTACT: Kirkness EF  
The Institute for Genomic Research  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.  
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Best Local Similarity 58.4%; Pred. No. 0.48;  
Matches 66; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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DB 292 TATTTTTCCTCAAGTTCAGGATCTTGTGGACCCAGGGATACCTCATTTTAA 233  
QY 105 ATCCATCTTACTCATGCACTTCATGCAACAGCAGCATATGTTTCTGTAAC 157  
DB 232 ATACATTTTATATGAAATTTTCAACACAAAATAAATGCTGTAGTAAAC 180

RESULT 7  
CO689495/c 643 bp mRNA linear EST 26-JUL-2004  
LOCUS CO689495  
DEFINITION Dg11-25n6 Dg11-kidney Canis familiaris cDNA 3', mRNA sequence.  
ACCESSION CO689495  
VERSION CO689495.1 GI:50638161  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

REFERENCE 1 (bases 1 to 643)  
AUTHORS Schluter, T., Hermanns, J., Weindel, M., Schuetz, D., Kranz, H.,  
Henrich, J. and Loebner, R.  
TITLE Dog arrayTAG cDNA clone collection  
JOURNAL Unpublished (2004)  
COMMENT Contact: Thomas Schuetz  
LION Bioscience AG  
Walhoferstrasse 98, D-69123 Heidelberg, Germany  
Tel: +49 6221 4038 150  
Fax: +49 6221 4038 290  
Email: Thomas.Schluter@lionbioscience.com.

FEATURES  
source  
1..643  
Location/Qualifiers

/organism="Canis familiaris"  
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Best Local Similarity 58.4%; Pred. No. 0.49;  
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DB 333 TATTTTTCCTCAAGTTCAGGATCTTGTGGACCCAGGGATACCTCATTTTAA 274  
QY 105 ATCCATCTTACTCATGCACTTCATGCAACAGCAGCATATGTTTCTGTAAC 157  
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RESULT 8  
AG366773/c 1085 bp DNA linear GSS 21-DEC-2004  
LOCUS AG366773  
DEFINITION Mus musculus molossinus DNA, clone:MSM01-170B12.TU, genomic survey  
sequence.  
ACCESSION AG366773  
VERSION AG366773.1 GI:47977978  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus (Japanese wild mouse)  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE 1  
AUTHORS Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwa, K. and  
Shiroishi, T.

TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to  
genomic constitution of strain C57BL/6J, as defined by BAC-end  
sequence-SNP analysis  
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)  
PUBMED 15574823

REFERENCE 2 (bases 1 to 1085)  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-2003) Masahiro Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
(E-mail: hattori@gsc.riken.jp, URL: http://ngp.gsc.riken.go.jp/  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT Clones are derived from the mouse BAC library MSM01. For BAC  
library availability, please contact Kunhya Abe (abe@rc.riken.jp).  
Tsukuba Institute, Bio Resource Center.  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rc.riken.jp

PRIMERS  
Sequencing : TU  
LIBRARY  
Vector : pBAC3.6  
R Site 1 : EcoRI  
R Site 2 : EcoRI.

FEATURES  
source  
1..1085  
Location/Qualifiers

/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSM01-170B12.TU"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_id="MSM01 Mouse Male BAC library"

# ORIGIN

Query Match 24.1%; Score 37.8; DB 10; Length 1085;  
Best Local Similarity 51.9%; Pred. No. 0.57;  
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 22 CTACATGCTGTTAACCCTTCTGTTTCATGTCGCAAGCTTGCCATTTCGAAC 81  
DB 719 CTCCTACT 660  
QY 82 AAGAGATACCTACTCTCCCAATCCATCTTACTCATGCACTTCATGCAACAGCA 141  
DB 659 ACATNAATPACNCCCCCNANNAACCAANNAACCCGCAATTTTNNANNAATPAA 600  
QY 142 CATATGTTTCTGTG 154  
DB 599 CAACCTTTTGTG 587

RESULT 9  
CZ727957 874 bp DNA linear GSS 25-JUL-2005  
LOCUS CZ727957  
DEFINITION OC\_Ba0055124.f OC\_Ba Oryza coarctata genomic clone OC\_Ba0055124  
5', genomic survey sequence.  
ACCESSION CZ727957  
VERSION CZ727957.1 GI:71136431  
KEYWORDS GSS.  
SOURCE Oryza coarctata (Porteresia coarctata)  
ORGANISM Oryza coarctata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharctoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 874)  
 AUTHORS Kim, H., Collura, K., Waisoteki, M., Byrne, M., Stum, D., Smart, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and Ming, R.  
 TITLE OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Rod A. Ming  
 Arizona Genomics Institute  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: rwm@genome.arizona.edu  
 PCR primers  
 FORWARD: TTA TAC GAC TCA CTA TAG GG  
 BACKWARD: CAC TCA TTA GCG ACC CCA  
 Plate: 0055 row: 1 column: 24  
 Seq primer: TTA TAC GAC TCA CTA TAG GG  
 Class: BAC ends  
 Location/Qualifiers  
 1..874  
 /organism="Oryza coarctata"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:77588"  
 /clone="OC\_Ba005124"  
 /tissue\_type="leaves"  
 /dev\_stage="mature"  
 /lab\_host="DH10B"  
 /clone\_1lb="OC\_Ba"  
 /note="Vector: pGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
 Query Match 22.7%; Score 35.6; DB 10; Length 874;  
 Best Local Similarity 78.6%; Pred. No. 2.7; Indels 1; Gaps 1;  
 Matches 55; Conservative 0; Mismatches 14

QY 64 CTTGCTTCTTCAACCAAGGATACCTACCTCCCAACATCATCTTACTGACAA 123  
 Db 778 CTTGCTTCTTCAACCAAGGATACCTACCTCCCAACATCATCTTACTGACAA 836

QY 124 CTTGCTTCA 133  
 Db 837 CTTGCTTCA 846

RESULT 10  
 BBS05306 700 bp mRNA linear EST 25-OCT-2001  
 LOCUS BBS05306 RIKEN full-length enriched, 10 days lactation, adult  
 DEFINITION female mammary gland Mus musculus cDNA clone D730002G06, mRNA  
 sequence.  
 ACCESSION BBS05306  
 VERSION BBS05306.2 GI:16442791  
 KEYWORDS EST  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus (house mouse)  
 REFERENCE Mammalia; Eutheria; Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 700)  
 Atakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,  
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,  
 Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,  
 Omo, H., Sasaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,  
 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,  
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
 Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
 Unpublished (2001)  
 On Jul 27, 2000 this sequence version replaced gi:9514268.  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Sushiro-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-resgsc.riken.jp, url: http://genome.gsc.riken.jp/  
 Carninci, P., Shibata, K., Hayashi, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10): 1617-1630 (2000)  
 waji, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,  
 Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.  
 and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multichannel sequencer. Genome Res.  
 10 (11): 1757-1771 (2000)  
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,  
 Sugahara, Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2): 281-289 (2001)  
 Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamana, I.,  
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
 Hayashizaki, Y.  
 Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome 12: 673-677 (2001)  
 please visit our web site (http://genome.gsc.riken.go.jp/) for  
 further details.  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Location/Qualifiers  
 1..700  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="D730002G06"  
 /sex="female"  
 /tissue\_type="mammary gland"  
 /dev\_stage="10 days lactation, adult"  
 /lab\_host="DH10B"  
 /clone\_1lb="RIKEN full-length enriched, 10 days lactation,  
 adult female mammary gland"  
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 Riken. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer 15GAGGATTTTCTTTTCTTTTCTTTTCTTTTCTTTT  
 3'. cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. Second strand cDNA was prepared with the  
 primer adapter of sequence 15'  
 GAGGAGAGATTTCTCGAGTTTAAATTAATATCCCCCCCCC 3'. cDNA  
 was cleaved with BamHI and XhoI. Vector: a modified  
 pBlueScript KS(+) after bulk excision from Lambda FIC 1."

ORIGIN  
 Query Match 21.7%; Score 34; DB 2; Length 700;  
 Best Local Similarity 54.9%; Pred. No. 8.3;  
 Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 27 TGGTTTCAACGCTTCCTGCTTCCTGCTTCGACGCTTCATTCGACCAAGG 86  
 Db 195 TCTTTTCTTCCCTCCCTCCCTGATTTCTTTGACCTGACCTTCATTTGGCTTAAGTT 254

QY 87 GATACCTACCTCCCAACATCATCTTACTGATGCACTTCATGCAACGACCATAT 146

Db	255	GTTCATGATTCCTCCAAAGACCATTTGGCACTACAGTCAAACATCATACACCTGAAAT	314
Qy	147	GT	148
Db	315	GT	316
RESULT 11			
LOCUS	CM871670	734 bp	DNA
DEFINITION	she2h3-44.g.013.ab1 Whole-genome shotgun library of the elephant shark (aka elephant fish) Callorhynchus milii genomic, genomic survey sequence.		
ACCESSION	CM871670		
VERSION	CM871670.1	GI:59698305	
KEYWORDS	GSS.		
SOURCE	Callorhynchus milii (elephantfish)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Callorhynchidae; Callorhynchus.		
REFERENCE	Holocephali; Chimaeriformes; Callorhynchidae; Callorhynchus.		
AUTHORS	1 (bases 1 to 734)		
TITLE	Venkatesh, B., Tay, A., Dandona, N., Patel, J. G. and Brenner, S.		
JOURNAL	A compact cartilaginous fish model genome		
PUBMED	Curr. Biol. 15 (3), R82-R83 (2005)		
COMMENT	15694293		
	Contact: Venkatesh B		
	Molecular Genetics Lab		
	Institute of Molecular and Cell Biology		
	61 Biopolis Drive, Singapore 138673		
	Tel: 65 6586 9571		
	Fax: 65 6779 1117		
	Email: mcbv@imcb.a-star.edu.sg		
	Whole-genome shotgun sequences of the elephant shark (aka elephant fish)		
FEATURES	Class: shotgun.		
source	Location/Qualifiers		
	1..734		
	/organism="Callorhynchus milii"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:7868"		
	/sex="Male"		
	/tissue_type="Testis"		
	/clone_lib="Whole-genome shotgun library of the elephant shark (aka elephant fish)"		
ORIGIN			
	Query Match	21.5%;	Score 33.8; DB 10; Length 734;
	Best Local Similarity	54.4%;	Pred. No. 9.8;
	Matches	68; Conservative	0; Mismatches 57; Indels 0; Gaps 0;
Qy	1	CGTGTGATCTGCATGCGATACATGATCATGCTGTGTCACCGTGTGTTGTCATGTC	60
Db	238	COTGGCAATTCATTTGCAATTTGCACTCCACGTATTTATGCACTGAACTTGTGTTAAATGACCC	179
Qy	61	AAGCTTGCCCTATTCTTGAAACCAAGAGATCTACTTCCCAACATTCATCTTACTGAC	120
Db	178	GAACTACACCAACCCACAGACACCAAGACATACACCAACCAACCATTTAACACAGA	119
Qy	121	CAACT	125
Db	118	AATCT	114
RESULT 12			
LOCUS	CL026582	1677 bp	DNA
DEFINITION	CH216-23G24_Sp6.1 CH216 Xenopus tropicalis genomic clone		
ACCESSION	CH216-23G24		
VERSION	CL026582		
KEYWORDS	CL026582.1	GI:40470443	
SOURCE	GSS.		
ORGANISM	Xenopus tropicalis (western clawed frog)		
	Xenopus tropicalis		

REFERENCE	TITLE	JOURNAL	COMMENT
AUTHORS			
REFERENCE			
1 (bases 1 to 1677)			
Kremetzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,			
Mardis, E., and Wilson, R.			
A physical map of the xenopus tropicalis genome			
Unpublished (2003)			
Contact: Richard K Wilson			
Genome Sequencing Center			
Washington University School of Medicine			
Email: submissions@watson.wustl.edu			
Insert Length: 175000 Std Error: 0.00			
Seq primer: Sp6 ATTAGGTGACACTATAG			
Class: BAC ends			
High quality sequence start: 125			
High quality sequence stop: 217.			
Location/Qualifiers			
1. 1677			
/organism="Xenopus tropicalis"			
/mol_type="genomic DNA"			
/strain="Nigerian frog"			
/db_xref="taxon:8364"			
/clone="CH216-23G24"			
/sex="male"			
/cell_line="Stock 248 F7A2, inbred N7"			
/clone_11b="CH216"			
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis			
BAC library"			
ORIGIN			
Query Match	21.4%	Score 33.6;	DB 10; Length 1677;
Best Local Similarity	53.9%	Pred. No. 15;	
Matches	69;	Conservative 0;	Mismatches 59; Indels 0; Gaps 0;
QY	3	TGTCATCTCAGTCAGTACTACATGCTGTTCAACCGTTCGTTGTTCCATGTCGCA	62
DB	769	TGTGCTCAGTCAGTACTACTCTGATTTCTTTGCTTCTATACATGTCATCGCGTT	828
QY	63	GCCTTGCTTATTTGGAACCAAGAGATTAAGTCTTCCCAACATCATCTTACTCATGCA	122
DB	829	TCATCACTATTTCTTACAGTTTCATGTCACCTCCTCCTCATCTTCTATATATTATTCAGACA	888
QY	123	ACTTCCAT 130	
DB	889	TCTTCCAT 896	
RESULT 13			
LOCUS	AT1744861	440 bp	mRNA linear EST 21-JUN-1999
DEFINITION	tr16b06.x1 NCI CGAP OV23 Homo sapiens cDNA clone IMAGE:2218451 3',		
ACCESSION	AT1744861		
VERSION	AT1744861.1	GI:5113149	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
REFERENCE	1 (bases 1 to 440)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
JOURNAL	Contact: Robert Strusberg, Ph.D.		
COMMENT	Email: cgsbbs-remail.nih.gov		
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.		
	Emmett-Buck, M.D., Ph.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www.bio.lnl.gov/bbr/image/image.html](http://www.bio.lnl.gov/bbr/image/image.html)

Seq primer: -400p from Gibco High quality sequence stop: 411.

## FEATURES

Location/Qualifiers

1..440  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2218451"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_1ib="NCI CGAP Ovi23"  
/note="Organ: ovary; Vector: PCMV-SPORE6; Site: 1; Salt: Site 2; NotI: Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"

## ORIGIN

Query Match Best Local Similarity 20.9%; Score 32.8; DB 1; Length 440;

Matches 61; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 46 CTGTTCCTGCTGCAAGCTTGGCTTATTCGACCAAGAGATCTACTCCCAACAA 105  
DB 259 CTTGGCCGCAACATGATATATATATATATATATATATATATATATATATAT 318  
QY 106 TCCATCTTACTCATGCACTTCATGCAACAGCAGCATATGTTTCT 153  
DB 319 TCCATCTTAAATTAACAGCTGATGTCCTGATATATCTTTTCT 366

## RESULT 14

CX446438

JGI\_XZG22009.rev NIH XGC trop667 Xenopus tropicalis cDNA clone

IMAGE:7537449.3', mRNA sequence.

CX446438

GI:57262270

EST.

Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

Xenopodidae; Xenopus; Silurana.

Richardson, P., Lucas, S., Rokear, D., Dettler, J. C., Ng, D. C.,

Brookstein, P. and Lindquist, E. A.

DOE Joint Genome Institute Xenopus tropicalis EST project

Unpublished (2004)

Other ESTs: JGI\_XZG22009.fwd

Contact: Lindquist, E. A., Richardson, P.

DOE Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Tel: 925 236 5600

Fax: 925 236 5710

Email: [cdna@jgi-psf.org](mailto:cdna@jgi-psf.org)

Tissue procurement: Richard M. Harland Laboratory, University of

California, Berkeley: <http://tropicalis.berkeley.edu/home>

cDNA Library Preparation: Richard M. Harland Laboratory, University

of California, Berkeley

DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>

Clone Distribution: I.M.A.G.E. Consortium/LNL:

<http://image.lnl.gov>

Naming Conventions: EST name is generated by the concatenation of

the JGI Clone id and the direction of sequencing. The suffix '.rev'

indicates a reverse sequencing read of the insert. It does not

necessarily reflect the orientation of the insert.

Poly-A: Based upon the presence of a run of 14 or more T residues

at the beginning of the sequence, this clone was polyadenylated.

## FEATURES

source

Location/Qualifiers

1..648  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7537449"  
/tissue\_type="whole embryo"  
/dev\_stage="Gastrula (st. 10.5-12.5)"  
/lab\_host="E. coli XL1-Blue derivative, Stratagene Electrogen-Blue"  
/clone\_1ib="NIH XGC trop667"  
/note="Vector: PCS108; Site: 1; Salt: Site 2; NotI: Gastrula library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen Superscript Plasmid System for cDNA synthesis and cloning). Salt (5' end) -NotI (3' end) cDNA was inserted into vector PCS108 (<http://mcb.berkeley.edu/labs/harland/pages/plasmids.html>)"

## ORIGIN

Query Match Best Local Similarity 20.9%; Score 32.6; DB 8; Length 648;

Matches 50; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 74 TTTGACCAAGAGATACCTTACCTCCCAACATCATCTTACTCATGCACTTCATGCA 133  
DB 586 TTGATGATTAAGAAAGGCGCATCTCCATAGACTCATTTTAGCGAAGTATTTCAATTT 527  
QY 134 AACAGCAATATGTTTCC 152  
DB 526 AAAAGTATTTTTTTTTC 508

## RESULT 15

CW558661/c

OA\_ABA0080807.f OA\_ABA Oryza australiensis genomic clone

CW558661

GI:54424196

SSS.

Oryza australiensis

Oryza australiensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehretidae; Oryza.

Kim, H., Yu, Y., Stum, D., Yeast, D., Rao, K., Luo, M., Jetty, R.,

Kudrna, D., Muller, C., Hatfield, D., Soderlund, C. and Wing, R.

OMP Project

Unpublished (2004)

Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: [twing@genome.arizona.edu](mailto:twing@genome.arizona.edu)

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG

BACKWARD: CAC TCA TTA GGC ACC CCA

Plate: 0080 row: B column: 07

Seq primer: TAA TAC GAC TCA CTA TAG GG

Class: BAC ends.

Location/Qualifiers

1..740

/organism="Oryza australiensis"

/mol\_type="genomic DNA"

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

## FEATURES

source

Location/Qualifiers

1..740

/organism="Oryza australiensis"

/mol\_type="genomic DNA"

/db\_xref="taxon:4532"  
/clone="OA\_Aba080807"  
/issue\_type="Young leaves"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_id="OA\_Aba"  
/note="Vector: pAGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

## ORIGIN

Query Match 20.8%; Score 32.6; DB 10; Length 740;  
Best Local Similarity 63.3%; Pred. No. 24;  
Matches 50; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
QY 79 ACCAAGAGATACCTACTCCCAACAATCCATCTTACTCATGCAACTTCATGCAACAC 138  
Db 653 ACCAATATTAATACTACTCCCAACAATGATCTTTCTTAAGCCAATGAAAGCAACAT 594  
QY 139 GCACATATGTTTCTCTGAAC 157  
Db 593 GCAACTGCGTGAGCTGAGC 575

Search completed: March 6, 2006, 01:57:49  
Job time : 742.207 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:54:12; Search time 43.8947 Seconds  
(without alignments)  
6357.883 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1155\_1311

Perfect score: 157  
Sequence: 1 cgtgcacatccacacgacatc.....cgcacatcgttcctgaac 157

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/1 COMB. seq:\*
- 2: /cgn2\_6/prodata/1/ina/5 COMB. seq:\*
- 3: /cgn2\_6/prodata/1/ina/6 COMB. seq:\*
- 4: /cgn2\_6/prodata/1/ina/6 COMB. seq:\*
- 5: /cgn2\_6/prodata/1/ina/6 COMB. seq:\*
- 6: /cgn2\_6/prodata/1/ina/6 COMB. seq:\*
- 7: /cgn2\_6/prodata/1/ina/6 COMB. seq:\*
- 8: /cgn2\_6/prodata/1/ina/6 COMB. seq:\*
- 9: /cgn2\_6/prodata/1/ina/6 COMB. seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	157	100.0	1394	US-08-880-499-1	Sequence 1, Appl 1
2	157	100.0	1394	US-08-880-499-2	Sequence 2, Appl 1
3	30.4	19.4	385136	US-09-949-016-16073	Sequence 16073, A
4	29.6	18.9	1185	US-09-543-681A-1081	Sequence 1081, Ap
5	29.2	18.6	1830121	US-09-557-884-1	Sequence 1, Appl 1
6	29.2	18.6	1830121	US-10-158-865-1	Sequence 1, Appl 1
7	28.2	18.3	64190	US-09-949-016-14712	Sequence 14712, A
8	28.8	18.3	64190	US-09-949-016-15502	Sequence 15502, A
9	28.8	18.3	64190	US-09-949-016-17447	Sequence 17447, A
10	28	17.8	11022	US-09-849-016-19101	Sequence 19101, A
11	27.8	17.7	601	US-09-849-016-14149	Sequence 14149, A
12	27.8	17.7	11490	US-09-849-016-14149	Sequence 16740, A
13	27.8	17.7	14952	US-09-849-016-16740	Sequence 16740, A
14	27.6	17.6	927	US-09-937-8628-37	Sequence 37, Appl 1
15	27.6	17.5	1413	US-09-110-279-1813	Sequence 1813, Ap
16	27.4	17.5	1413	US-09-134-001C-1413	Sequence 1413, Ap
17	27.4	17.5	1428	US-09-270-767-10489	Sequence 10489, A
18	27.4	17.5	1794	US-08-425-299A-2	Sequence 2, Appl 1
19	27.4	17.5	2472	US-09-710-279-3747	Sequence 3747, Ap
20	27.4	17.5	2926	US-09-710-279-3680	Sequence 3680, Ap
21	27.4	17.5	3014	US-09-710-279-4003	Sequence 4003, Ap
22	27.2	17.3	3599	US-09-949-016-2556	Sequence 2556, Ap
23	27.2	17.3	3445	US-09-949-016-2556	Sequence 2556, Ap
24	27.2	17.3	3588	US-09-566-921-23	Sequence 23, Appl 1

25	27.2	17.3	6751	US-07-882-925A-5	Sequence 5, Appl 1
26	27.2	17.3	6751	US-08-184-012C-5	Sequence 5, Appl 1
27	27.2	17.3	8939	US-09-949-016-12703	Sequence 12703, A
28	27.2	17.3	9076	US-09-949-016-17368	Sequence 17368, A
29	27.2	17.3	48994	US-09-949-016-14091	Sequence 14091, A
30	27.2	17.3	60593	US-09-949-016-13779	Sequence 13779, A
31	27.2	17.3	62776	US-09-949-016-1576	Sequence 1576, A
32	27.2	17.3	100848	US-09-596-002-39	Sequence 39, Appl 1
33	27.2	17.3	158735	US-09-949-016-11989	Sequence 11989, A
34	27.2	17.3	158735	US-09-949-016-17130	Sequence 17130, A
35	27.2	17.3	879	US-09-949-016-12088	Sequence 12088, A
36	27	17.2	44180	US-09-949-016-15040	Sequence 15040, A
37	27	17.2	47030	US-09-949-016-15038	Sequence 15038, A
38	27	17.2	47030	US-09-949-016-15038	Sequence 15038, A
39	27	17.2	47030	US-09-949-016-15040	Sequence 15040, A
40	27	17.2	160552	US-09-593-828-11	Sequence 11, Appl 1
41	27	17.2	194537	US-09-949-016-12928	Sequence 12928, A
42	27	17.2	201529	US-09-949-016-12740	Sequence 12740, A
43	26.8	17.1	265	US-09-513-999C-8379	Sequence 8379, Ap
44	26.8	17.1	271	US-08-946-026-9	Sequence 9, Appl 1
45	26.8	17.1	271	US-08-946-026-9	Sequence 9, Appl 1

## ALIGNMENTS

RESULT 1  
US-08-880-499-1  
Sequence 1, Application US/08880499  
Patent No. 6037523

GENERAL INFORMATION:  
APPLICANT: Albertson, Marc C.  
APPLICANT: Fox, Tim W.  
APPLICANT: Carl, Garnaat W.  
APPLICANT: Hufman, Gary A.  
APPLICANT: Kendall, Timmy L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION  
TITLE OF INVENTION: AND METHOD OF USING SAME  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.  
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.  
STREET: Box 1000  
CITY: Johnston  
STATE: Iowa  
COUNTRY: USA  
ZIP: 50131

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,499  
FILING DATE: CONCURRENTLY HERewith  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sweeney, Patricia A.  
REGISTRATION NUMBER: 32,733  
REFERENCE/DOCKET NUMBER: 0578  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (515) 248-4800  
TELEFAX: (515) 248-4844  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1394 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-880-499-1

Query Match 100.0%; Score 157; DB 3; Length 1394;

Best Local Similarity 100.0%; Pred. No. 9,4e-44;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGTACATCTACATGATCTACATGCTTGTCAACCGTTGCTTGTTCATCGTC 60  
Db 1155 CGTGTACATCTACATGATCTACATGCTTGTCAACCGTTGCTTGTTCATCGTC 1214

Qy 61 AAGCTTGCTTATCTGTAACGAGATGATCTACTCCCAACATCCATCTACTCATG 120  
Db 1215 AAGCTTGCTTATCTGTAACGAGATGATCTACTCCCAACATCCATCTACTCATG 1274

Qy 121 CAACTTCATGCAAAACGACACATATGTTCTCTGAAC 157  
Db 1275 CAACTTCATGCAAAACGACACATATGTTCTCTGAAC 1311

RESULT 2  
US-08-880-499-2  
Sequence 2, Application US/08880499  
Patent No. 6037523  
GENERAL INFORMATION:  
APPLICANT: Albertson, Marc C.  
APPLICANT: Fox, Tim W.  
APPLICANT: Carl, Garnat W.  
APPLICANT: Huffman, Gary A.  
APPLICANT: Kendall, Timmy L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION  
TITLE OF INVENTION: AND METHOD OF USING SAME  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.  
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.  
CITY: Johnston  
STATE: Iowa  
COUNTRY: USA  
ZIP: 50131  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,499  
FILING DATE: CONCURRENTLY HEREWITH  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sweeney, Patricia A.  
REGISTRATION NUMBER: 32,733  
REFERENCE/DOCKET NUMBER: 0578  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (515) 248-4800  
TELEFAX: (515) 248-4844  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1394 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-880-499-2

Query Match 100.0%; Score 157; DB 3; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 9,4e-44;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 CAACTTCATGCAAAACGACACATATGTTCTCTGAAC 157  
Db 1275 CAACTTCATGCAAAACGACACATATGTTCTCTGAAC 1311

RESULT 3  
US-09-949-016-16073/c  
Sequence 16073, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16073  
LENGTH: 385136  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(385136)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-16073

Query Match 19.4%; Score 30.4; DB 3; Length 385136;  
Best Local Similarity 57.3%; Pred. No. 14;  
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 55 TCGTCAAGCCTTGCTTATCTGTAACGAGATGATCTCTCCCAACATCATCTTA 114  
Db 25308 TCGTCAAGCCTTGCTTATCTGTAACGAGATGATCTCTCCCAACATCATCTTA 253849

Qy 115 CTCATGCACTTCCATGCAAAACGACACATATGTTT 150  
Db 253848 TCCATTTTATCTCCCAACGACACATTTT 253813

RESULT 4  
US-09-543-681A-1081/c  
Sequence 1081, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETTON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709,1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 1081  
LENGTH: 1185  
TYPE: DNA  
ORGANISM: Proteus mirabilis  
US-09-543-681A-1081

Query Match 18.9%; Score 29.6; DB 3; Length 1185;  
Best Local Similarity 59.5%; Pred. No. 3.4;  
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 35 CAACGTTGCTTGTTCATGTCGAAGCCTTATCTGTAACGAAGATACCTTA 94

Db 940 CACACATTTTGTTCACCAAGAAAGCTTACCCATTTTCTCCCAAGACATATCA 881  
QY 95 CTCCCAACATTCATTTACTCA 118  
Db 880 ATCCCTGAGATGCTTTTAAATA 857

RESULT 5  
US-09-557-884-1/c

; Sequence 1, Application US/09557884  
; Patent No. 6506581

## GENERAL INFORMATION:

APPLICANT: Fleischmann et al.  
TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION NUMBER: US/09/557,884  
APPLICATION NUMBER: 25-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,102  
FILING DATE: JUN-5-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB186F3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

Query Match 18.6%; Score 29.2; DB 3; Length 1830121;  
Best Local Similarity 51.5%; Pred. No. 63;  
Matches 67; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 12 ACATGCACTACATGCTTGTTCACCGTTCCTTGTTCACATGTCACAGCTTGCT 71  
Db 677275 ACTTAAATTCAGCTGCTGCTGCTCTATTCATTTGCAATTAATGCAACATAGCT 677216  
QY 72 ATTCTGAACCAAGAGATACCTTCTCCCAACATTCATCTTACTCATGCACTTCATG 131  
Db 677215 ATGCTGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 677156  
QY 132 CAACACGCA 141  
Db 677155 CAACCAACCA 677146

RESULT 6  
US-09-643-990A-1/c  
; Sequence 1, Application US/09643990A

Patent No. 6528289  
GENERAL INFORMATION:  
APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith  
J. Craig Venter

TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville,  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A  
FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426,787  
FILING DATE: 1995-04-21

## ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB186P1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 301-309-8439

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

Query Match 18.6%; Score 29.2; DB 3; Length 1830121;  
Best Local Similarity 51.5%; Pred. No. 63;  
Matches 67; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 12 ACATGCACTACATGCTTGTTCACCGTTCCTTGTTCACATGTCACAGCTTGCT 71  
Db 677275 ACTTAAATTCAGCTGCTGCTGCTCTATTCATTTGCAATTAATGCAACATAGCT 677216  
QY 72 ATTCTGAACCAAGAGATACCTTCTCCCAACATTCATCTTACTCATGCACTTCATG 131  
Db 677215 ATGCTGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 677156  
QY 132 CAACACGCA 141  
Db 677155 CAACCAACCA 677146

RESULT 7  
US-10-158-865-1/c  
; Sequence 1, Application US/10158865  
; Patent No. 6846651  
; GENERAL INFORMATION:  
APPLICANT: Fleischmann et al.  
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag  
; Patent No. 6846651

```

1 TITLE OF INVENTION: Therectf, and Uses Thereof
2 FILE REFERENCE: PH186PCCD1
3 CURRENT APPLICATION NUMBER: US/10/158,865
4 PRIOR FILING DATE: 2002-06-03
5 PRIOR APPLICATION NUMBER: US 09/557,884
6 PRIOR FILING DATE: 2000-04-25
7 PRIOR APPLICATION NUMBER: US 08/476,102
8 PRIOR FILING DATE: 1995-06-07
9 PRIOR APPLICATION NUMBER: US 08/426,787
10 PRIOR FILING DATE: 1995-04-21
11 NUMBER OF SEQ ID NOS: 1
12 SOFTWARE: PatentIn version 3.1
13 SEQ ID NO 1
14 LENGTH: 1830121
15 TYPE: DNA
16 ORGANISM: Haemophilus influenzae
17 FEATURE:
18 NAME/KEY: misc_feature
19 LOCATION: (4747)..(4747)
20 OTHER INFORMATION: n equals a,t,c, or g
21 FEATURE:
22 NAME/KEY: misc_feature
23 LOCATION: (19921)..(19921)
24 OTHER INFORMATION: n equals a,t,c, or g
25 FEATURE:
26 NAME/KEY: misc_feature
27 LOCATION: (10150)..(10150)
28 OTHER INFORMATION: n equals a,t,c, or g
29 FEATURE:
30 NAME/KEY: misc_feature
31 LOCATION: (29298)..(29298)
32 OTHER INFORMATION: n equals a,t,c, or g
33 FEATURE:
34 NAME/KEY: misc_feature
35 LOCATION: (36551)..(36551)
36 OTHER INFORMATION: n equals a,t,c, or g
37 FEATURE:
38 NAME/KEY: misc_feature
39 LOCATION: (36543)..(36543)
40 OTHER INFORMATION: n equals a,t,c, or g
41 FEATURE:
42 NAME/KEY: misc_feature
43 LOCATION: (36636)..(36636)
44 OTHER INFORMATION: n equals a,t,c, or g
45 FEATURE:
46 NAME/KEY: misc_feature
47 LOCATION: (40810)..(40810)
48 OTHER INFORMATION: n equals a,t,c, or g
49 FEATURE:
50 NAME/KEY: misc_feature
51 LOCATION: (4416)..(4416)
52 OTHER INFORMATION: n equals a,t,c, or g
53 FEATURE:
54 NAME/KEY: misc_feature
55 LOCATION: (44905)..(44905)
56 OTHER INFORMATION: n equals a,t,c, or g
57 FEATURE:
58 NAME/KEY: misc_feature
59 LOCATION: (44975)..(44975)
60 OTHER INFORMATION: n equals a,t,c, or g
61 FEATURE:
62 NAME/KEY: misc_feature
63 LOCATION: (45593)..(45593)
64 OTHER INFORMATION: n equals a,t,c, or g
65 FEATURE:
66 NAME/KEY: misc_feature
67 LOCATION: (45732)..(45732)
68 OTHER INFORMATION: n equals a,t,c, or g
69 FEATURE:
70 NAME/KEY: misc_feature
71 LOCATION: (47036)..(47036)
72 OTHER INFORMATION: n equals a,t,c, or g
73 FEATURE:
74 NAME/KEY: misc_feature
75 LOCATION: (47036)..(47036)
76 OTHER INFORMATION: n equals a,t,c, or g
77 FEATURE:
78 NAME/KEY: misc_feature
79 LOCATION: (47036)..(47036)
80 OTHER INFORMATION: n equals a,t,c, or g
81 FEATURE:
82 NAME/KEY: misc_feature
83 LOCATION: (47036)..(47036)
84 OTHER INFORMATION: n equals a,t,c, or g
85 FEATURE:
86 NAME/KEY: misc_feature
87 LOCATION: (47036)..(47036)
88 OTHER INFORMATION: n equals a,t,c, or g
89 FEATURE:
90 NAME/KEY: misc_feature
91 LOCATION: (47036)..(47036)
92 OTHER INFORMATION: n equals a,t,c, or g
93 FEATURE:
94 NAME/KEY: misc_feature
95 LOCATION: (47036)..(47036)
96 OTHER INFORMATION: n equals a,t,c, or g
97 FEATURE:
98 NAME/KEY: misc_feature
99 LOCATION: (47036)..(47036)
100 OTHER INFORMATION: n equals a,t,c, or g

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NAME/KEY: misc_feature	LOCATION: (513344) ..(513344)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (51602) ..(51602)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (51786) ..(51786)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (53569) ..(53569)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (65309) ..(65309)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (65313) ..(65313)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (80024) ..(80024)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (100091) ..(100091)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (102696) ..(102696)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (105121) ..(105121)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (107248) ..(107248)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (11924) ..(11924)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (119750) ..(119750)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (120038) ..(120038)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (121344) ..(121344)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		
NAME/KEY: misc_feature	LOCATION: (122167) ..(122167)	OTHER INFORMATION: n equals a,t,c, or g
FEATURE:		



GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03/237,768  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15502  
LENGTH: 11022  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-15502

Query Match 17.8%; Score 28; DB 3; Length 11022;  
Best Local Similarity 63.2%; Pred. No. 27;  
Matches 43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 15 TGGCATCTACATGCTTGTCAACCGTTCCTTGTTCATGTCACCGCTTCTATT 74  
DB 4432 TGGCTATTTCATGCTGTTTGTAGGTTATGTTGATGATTCATTAGCTTGTCAAG 4491

QY 75 CTGAACCA 82  
DB 4492 CTGAATCA 4499

RESULT 11  
US-09-949-016-17447  
Sequence 17447, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17447  
LENGTH: 41815  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-17447

Query Match 17.8%; Score 28; DB 3; Length 41815;  
Best Local Similarity 58.3%; Pred. No. 43;  
Matches 49; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 62 AGCCTTGGCTTATTCGACCAAGAGATACCTACCTCCCAACATCATTACTATGC 121  
DB 33058 AGACATGAGATGACACACATCCGATGCTGCTTACGAGATCCCTGGTCACTATTC 33117

QY 122 AACTTCATGCAACGACCATTA 145  
DB 33118 ATGTACATAGAGACATGATTA 33141

RESULT 12

US-09-949-016-191201/c  
Sequence 191201, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 191201  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-191201

Query Match 17.7%; Score 27.8; DB 3; Length 601;  
Best Local Similarity 58.0%; Pred. No. 11;  
Matches 47; Conservative 1; Mismatches 33; Indels 0; Gaps 0;

QY 57 GTCCAGCCTTGCTTATTCGACCAAGAGATACCTACCTCCCAACATCATTACT 116  
DB 322 GTCCAGCTTGATGACACACATGACGCGCACCAACACACACACATCTCTTCTATT 263

QY 117 CATGCACTTCATGCAACA 137  
DB 262 CATGCAATAGAGATGAATA 242

RESULT 13  
US-09-949-016-14149/c  
Sequence 14149, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14149  
LENGTH: 11490  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-14149

Query Match 17.7%; Score 27.8; DB 3; Length 11490;  
Best Local Similarity 52.1%; Pred. No. 32;  
Matches 62; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 38 CCGTTGCTTGTTCATGTCACAGCTTGCCTATTCTGAACCAAGAGATACCTACTC 97  
DB 5642 CAGGCGCTTCTGCTCCGCGCCCTCCCTCCCACTCACAGGAGGAGCCACGC 5583

QY 98 CCAACATCATCTTACTGATGACATCTTCACCAACAGGACATATGTTTCTGTA 156  
DB 5582 CTTGACACCTGATGACCATTCGCTTGAAGTGGCAGGAGTGAAGATGTTGCCAATA 5524

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RESULT 14
US-09-949-016-16740
; Sequence 16740, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16740
; LENGTH: 14952
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16740

Query Match      17.7%; Score 27.8; DB 3; Length 14952;
Best Local Similarity 59.5%; Pred. No. 35;
Matches 47; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY      67  TGCCTATTTCGACCAAGAGATACCTACTCCCAACATCCATCTTACTGATCAACTT 126
Db      70  TGTCAACCGTATCTCAACAGTATATTAGTTCTAGAAATTCCTCTCCACAGTAACTA 129
QY      127 CCATGCAACACGACACATA 145
Db      130 GGTTTTACACACACACACA 148

RESULT 15
US-09-937-862B-37
; Sequence 37, Application US/09937862B
; Patent No. 6846621
; GENERAL INFORMATION:
; APPLICANT: Oberste, M. Steven
; APPLICANT: Maher, Kaija
; APPLICANT: Kilpatrick, David R.
; APPLICANT: Ballantrich, Mark A.
; TITLE OF INVENTION: TYPING OF HUMAN ENTEROVIRUSES
; FILE REFERENCE: 14114.035302
; CURRENT APPLICATION NUMBER: US/09/937,862B
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: PCT/US00/07828
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/127,464
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. 6846621e =
; OTHER INFORMATION: synthetic construct
US-09-937-862B-37

Query Match      17.6%; Score 27.6; DB 3; Length 927;
Best Local Similarity 55.1%; Pred. No. 15;
Matches 54; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY      53  CATGTCGACGCTTGCCTATTTCGACCAAGAGATACCTACTCCCAACATTCATCT 112

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Db      551  CATCATCAAAACCCCTCAATATTCTACCTATGGAACGACACCCAGATTTCATCC 610
QY      113  TACTATGCAACTTCCATGCAACACGACCATATGTTT 150
Db      611  CTTTGTGGGATTACAAACGGATCTCAATTTTAT 648

Search completed: March 5, 2006, 22:36:28
Job time : 46.8947 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: March 5, 2006, 23:29:31 ; Search time 225.751 Seconds  
(Without alignments)  
5750.985 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1155\_1311

Perfect score: 157  
Sequence: 1 CGTGTCTTCATCAGCAAGCAATGTTCTTCGTAAC 157

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications NA Main:  
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2: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*  
3: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*  
4: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
5: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
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7: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
8: /cgn2\_6/prodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
9: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	157	100.0	1394	8	US-10-713-381-2
4	146	93.0	158	8	US-10-713-381-3
5	50	31.8	50	8	US-10-713-381-5
6	40	25.5	40	8	US-10-713-381-6
7	32.2	20.5	399	8	US-10-674-124A-9081
8	31.4	20.1	2352	7	US-10-282-123A-36272
9	31.6	20.1	565	4	US-09-925-065A-871704
10	30.8	19.6	601	4	US-09-925-065A-871704
11	30.8	19.6	1122	7	US-10-437-963-1496
12	30.6	19.5	553	5	US-10-027-632-244811
13	30.6	19.5	553	5	US-10-027-632-244811
14	30.6	19.5	79467	7	US-10-027-632-244811
15	30.4	19.4	52001	7	US-10-317-771-11
16	30.2	19.2	436	4	US-09-925-065A-153052
17	30.2	19.2	1266	9	US-10-501-282-2923
18	30.2	19.2	1266	9	US-10-501-282-2923
19	30	19.1	30	8	US-10-713-381-4
20	30	19.1	843	5	US-10-027-632-170626
21	30	19.1	843	5	US-10-027-632-170626
22	29.8	19.0	236	6	US-09-783-590-10490
23	29.8	19.0	617	4	US-09-925-065A-285326

24	29.8	19.0	617	4	US-09-925-065A-285327	Sequence 285327, A
25	29.8	19.0	617	4	US-09-925-065A-285328	Sequence 285328, A
26	29.8	19.0	691	7	US-10-424-599-57038	Sequence 57038, A
27	29.8	19.0	1363	4	US-09-925-065A-12385	Sequence 12385, A
28	29.8	19.0	2735	5	US-10-027-632-254612	Sequence 254612, A
29	29.8	19.0	2735	5	US-10-027-632-254612	Sequence 254612, A
30	29.8	19.0	1223197	6	US-10-027-632-179264	Sequence 179264, A
31	29.8	18.9	680	7	US-10-767-701-2154	Sequence 2154, A
32	29.6	18.9	1475	6	US-10-329-670-1	Sequence 1, Appli
33	29.2	18.6	1830121	7	US-10-329-670-1	Sequence 1, Appli
34	29.2	18.6	1830121	8	US-10-158-865-1	Sequence 1, Appli
35	29.2	18.6	1830121	9	US-10-981-687-1	Sequence 78606, A
36	29.2	18.5	358	8	US-10-425-115-78606	Sequence 22244, A
37	29	18.5	553	5	US-10-027-632-222445	Sequence 222445, A
38	29	18.5	553	5	US-10-027-632-222445	Sequence 222445, A
39	29	18.5	553	6	US-10-027-632-222445	Sequence 222445, A
40	29	18.5	553	6	US-10-027-632-222445	Sequence 222445, A
41	29	18.5	7192	7	US-10-437-963-85365	Sequence 85365, A
42	29	18.5	544	4	US-09-925-065A-805392	Sequence 805392, A
43	28.8	18.3	732	5	US-10-027-632-21721	Sequence 21721, A
44	28.8	18.3	732	5	US-10-027-632-21721	Sequence 21721, A
45	28.8	18.3	732	5	US-10-027-632-21722	Sequence 21722, A

#### ALIGNMENTS

RESULT 1  
US-10-713-381-9  
Sequence 9, Application US/10713381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUPFMAN, GARY  
APPLICANT: KENALL, TIMMY L.  
TITLE OR INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
TITLE OR INVENTION: USING SAME  
FILE REFERENCE: 578R  
CURRENT FILING DATE: US/10/713,381  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 255  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-9  
Query Match 100.0%; Score 157; DB 8; Length 255;  
Best Local Similarity 100.0%; Pred No. 2.1e-43;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTGTCTTCATCAGCAAGCAATGTTCTTCGTAAC 60  
DB 15 CGTGTCTTCATCAGCAAGCAATGTTCTTCGTAAC 74  
QY 61 AAGCTTCCCTATTCGAAAGCAAGATATCTCCCAAAATTCATCTTACATG 120  
DB 75 AAGCTTCCCTATTCGAAAGCAAGATATCTCCCAAAATTCATCTTACATG 134  
QY 121 CAATTCATGCAAGCAAGCAATGTTCTTCGTAAC 157  
DB 135 CAATTCATGCAAGCAAGCAATGTTCTTCGTAAC 171  
RESULT 2  
US-10-713-381-1  
Sequence 1, Application US/10713381  
Publication No. US20040221331A1

GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1394  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-1

Query Match 100.0%; Score 157; DB 8; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 3.8e-43;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGCATCTCAGATGCGATCTACATGCTGTTCACCGCTTCCTGTCATCGTCC 60

Db 1155 CGTGCATCTCAGATGCGATCTACATGCTGTTCACCGCTTCCTGTCATCGTCC 1214

Qy 61 AAGCCTTGCTATTCTGTAACCAAGAGATACCTTACCCCAACATCCATCTTACTCATG 120

Db 1215 AAGCCTTGCTATTCTGTAACCAAGAGATACCTTACCCCAACATCCATCTTACTCATG 1274

Qy 121 CAATTCATGCAACACGACATATGTTCTCTGAAC 157

Db 1275 CAATTCATGCAACACGACATATGTTCTCTGAAC 1311

## RESULT 3

US-10-713-381-2  
Sequence 2, Application US/10713381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 1394  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-2

Query Match 100.0%; Score 157; DB 8; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 3.8e-43;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGCATCTCAGATGCGATCTACATGCTGTTCACCGCTTCCTGTCATCGTCC 60

Db 1155 CGTGCATCTCAGATGCGATCTACATGCTGTTCACCGCTTCCTGTCATCGTCC 1214

Qy 61 AAGCCTTGCTATTCTGTAACCAAGAGATACCTTACCCCAACATCCATCTTACTCATG 120

Db 1215 AAGCCTTGCTATTCTGTAACCAAGAGATACCTTACCCCAACATCCATCTTACTCATG 1274

Qy 121 CAATTCATGCAACACGACATATGTTCTCTGAAC 157

Db 1275 CAATTCATGCAACACGACATATGTTCTCTGAAC 1311

## RESULT 4

US-10-713-381-3  
Sequence 3, Application US/10713381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 158  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-3

Query Match 93.0%; Score 146; DB 8; Length 158;  
Best Local Similarity 99.4%; Pred. No. 1e-39;  
Matches 157; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGTGCATCTCAGATGCGATCTACATGCTGTTCACCGCTTCCTGTCATCGTCC 59

Db 1 CGTGCATCTCAGATGCGATCTACATGCTGTTCACCGCTTCCTGTCATCGTCC 60

Qy 60 CAAGCCTTGCTATTCTGTAACCAAGAGATACCTTACCCCAACATCCATCTTACTCAT 119

Db 61 CAAGCCTTGCTATTCTGTAACCAAGAGATACCTTACCCCAACATCCATCTTACTCAT 120

Qy 120 GCAATTCATGCAACACGACATATGTTCTCTGAAC 157

Db 121 GCAATTCATGCAACACGACATATGTTCTCTGAAC 158

## RESULT 5

US-10-713-381-5  
Sequence 5, Application US/10713381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-5

Query Match 31.8%; Score 50; DB 8; Length 50;  
Best Local Similarity 100.0%; Pred. No. 5.7e-07;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 CTGACCAAGAGATCTACTCTCCCAACATCCATCTTACTCATGCAAC 124  
DB 1 CTGACCAAGAGATCTACTCTCCCAACATCCATCTTACTCATGCAAC 50

RESULT 6  
US-10-713-381-6

/ Sequence 6, Application US/10713381  
/ Publication No. US20040221331A1  
/ GENERAL INFORMATION:  
/ APPLICANT: ALBERTSEN, MARC C.  
/ APPLICANT: FOX, TIMOTHY W.  
/ APPLICANT: GARNAAT, CARL W.  
/ APPLICANT: HUFFMAN, GARY  
/ APPLICANT: KENDALL, TIMMY L.  
/ TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
/ FILE REFERENCE: 578R  
/ CURRENT APPLICATION NUMBER: US/10/713,381  
/ PRIOR FILING DATE: 2003-11-14  
/ PRIOR APPLICATION NUMBER: 08/680,499  
/ NUMBER OF SEQ ID NOS: 24  
/ SOFTWARE: Patent Ver. 2.0  
/ SEQ ID NO 6  
/ LENGTH: 40  
/ TYPE: DNA  
/ ORGANISM: Zea mays  
US-10-713-381-6

Query Match 25.5%; Score 40; DB 8; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AGGATACCTACTCTCCCAACATCCATCTTACTCATGCAAC 124  
DB 1 AGGATACCTACTCTCCCAACATCCATCTTACTCATGCAAC 40

RESULT 7

US-10-674-124A-9081/c  
/ Sequence 9081, Application US/10674124A  
/ Publication No. US2004019797A1  
/ GENERAL INFORMATION:  
/ APPLICANT: INOMO, Hidetoshi  
/ APPLICANT: TAMURA, Gen  
/ TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE  
/ FILE REFERENCE: ORIN-003C1P  
/ CURRENT APPLICATION NUMBER: US/10/674,124A  
/ PRIOR FILING DATE: 2003-09-26  
/ PRIOR APPLICATION NUMBER: 10/257,511  
/ PRIOR FILING DATE: 2003-03-07  
/ PRIOR APPLICATION NUMBER: PCT/JP00/07621  
/ PRIOR FILING DATE: 2000-10-30  
/ PRIOR APPLICATION NUMBER: JP2000-112699  
/ PRIOR FILING DATE: 2000-04-13  
/ PRIOR APPLICATION NUMBER: JP2002-327516  
/ PRIOR FILING DATE: 2002-09-28  
/ PRIOR APPLICATION NUMBER: JP2002-383869  
/ PRIOR FILING DATE: 2002-12-09  
/ NUMBER OF SEQ ID NOS: 27110  
/ SEQ ID NO 9081  
/ LENGTH: 399  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ OTHER INFORMATION: chr5.fa.07fzr.139538206

FEATURE:

OTHER INFORMATION: Located on chromosome 5

FEATURE:

OTHER INFORMATION: Distance between a terminus base of telomere on  
OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base

FEATURE: sequence : 128437212

FEATURE:

OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
OTHER INFORMATION: sequence listing upwards to telomere on chromosomal short arm and  
OTHER INFORMATION: 5'-terminus of this base sequence : 250186  
US-10-674-124A-9081

Query Match 20.5%; Score 32.2; DB 8; Length 399;  
Best Local Similarity 61.2%; Pred. No. 1.6e-33;  
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 72 ATTCTGAACCAAGAGATCTACTCTCCCAACATCCATCTTACTCATGCAACTTCGATG 131  
DB 239 ATTCTGAACCAAGAGATCTACTCTCCCAACATCCATCTTACTCATGCAACTTCGATG 180

QY 132 CAACACGACATATGTCTCTGAA 156  
DB 179 AAAAAACCAACATTTGTGATGAA 155

RESULT 8  
US-10-282-122A-36272/c

/ Sequence 36272, Application US/10282122A  
/ Publication No. US20040029129A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Wang, Liangsu  
/ APPLICANT: Zamudio, Carlos  
/ APPLICANT: Malone, Cheryl  
/ APPLICANT: Haselbeck, Robert  
/ APPLICANT: Ohlsson, Kari  
/ APPLICANT: Zvejdich, Judith  
/ APPLICANT: Wall, Daniel  
/ APPLICANT: Treweek, John  
/ APPLICANT: Carr, Grant  
/ APPLICANT: Yamamoto, Robert  
/ APPLICANT: Forsyth, R.  
/ APPLICANT: Xu, H.  
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
/ FILE REFERENCE: ELITPA.034A  
/ CURRENT APPLICATION NUMBER: US/10/282,122A  
/ PRIOR FILING DATE: 2003-02-20  
/ PRIOR APPLICATION NUMBER: 60/191,078  
/ PRIOR FILING DATE: 2000-03-21  
/ PRIOR APPLICATION NUMBER: 60/206,848  
/ PRIOR FILING DATE: 2000-05-23  
/ PRIOR APPLICATION NUMBER: 60/207,727  
/ PRIOR FILING DATE: 2000-05-26  
/ PRIOR APPLICATION NUMBER: 60/230,335  
/ PRIOR FILING DATE: 2000-09-06  
/ PRIOR APPLICATION NUMBER: 60/230,347  
/ PRIOR FILING DATE: 2000-09-09  
/ PRIOR APPLICATION NUMBER: 60/242,578  
/ PRIOR FILING DATE: 2000-10-23  
/ PRIOR APPLICATION NUMBER: 60/253,625  
/ PRIOR FILING DATE: 2000-11-27  
/ PRIOR APPLICATION NUMBER: 60/257,931  
/ PRIOR FILING DATE: 2000-12-22  
/ PRIOR APPLICATION NUMBER: 60/267,636  
/ PRIOR FILING DATE: 2001-02-09  
/ PRIOR APPLICATION NUMBER: 60/269,308  
/ PRIOR FILING DATE: 2001-02-16  
/ Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 78614  
/ SOFTWARE: Patent Ver. 3.1  
/ SEQ ID NO 36272  
/ LENGTH: 2352  
/ TYPE: DNA  
/ ORGANISM: Streptococcus mutans

; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092

RESULT 12  
US-10-027-632-244811  
; Sequence 244811, Application US/10027632

; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092

RESULT 12  
US-10-027-632-244811  
; Sequence 244811, Application US/10027632

```
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIORITY FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIORITY FILING DATE: 2000-07-12
PRIORITY APPLICATION NUMBER: US 60/198,676
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIORITY FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIORITY FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 244811
LENGTH: 559
TYPE: DNA
ORGANISM: Human
US-10-027-632-244811

Query Match
Best Local Similarity 51.9%; Score 30.6; DB 5; Length 559;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 24 ACATGCTGTTCAACCGTCTCTGTTCCATGTCGACCGCTGCTATTGTAACCAA 83
DB 380 ACATGCTGTTCAACCGTCTCTGTTCCATGTCGACCGCTGCTATTGTAACCAA 439
QY 84 GAGATACCTTACCTCCCAACATCCATCTTACTCATGCACTTCATGCAACAGCCACA 143
DB 440 TCTGCTCCCTTACCTTAAAGATTCATGAGAGTCTCTCAAAATCCATAGACACCTGAC 499
QY 144 TATGTTCTCTGAA 156
DB 500 ATTTCTTCCCA 512

RESULT 13
US-10-027-632-244811
Sequence 244811, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIORITY FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIORITY FILING DATE: 2000-07-12
PRIORITY APPLICATION NUMBER: US 60/198,676
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIORITY FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIORITY FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
NUMBER OF SEQ ID NOS: 325720
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 244811
LENGTH: 559
TYPE: DNA
ORGANISM: Human
US-10-027-632-244811

Query Match
Best Local Similarity 51.9%; Score 30.6; DB 6; Length 559;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 24 ACATGCTGTTCAACCGTCTCTGTTCCATGTCGACCGCTGCTATTGTAACCAA 83
DB 380 ACATGCTGTTCAACCGTCTCTGTTCCATGTCGACCGCTGCTATTGTAACCAA 439
QY 84 GAGATACCTTACCTCCCAACATCCATCTTACTCATGCACTTCATGCAACAGCCACA 143
DB 440 TCTGCTCCCTTACCTTAAAGATTCATGAGAGTCTCTCAAAATCCATAGACACCTGAC 499
QY 144 TATGTTCTCTGAA 156
DB 500 ATTTCTTCCCA 512

RESULT 14
US-10-052-482-223
Sequence 223, Application US/10052482
Publication No. US2004007264A1
GENERAL INFORMATION:
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71087/BMS/DCP
CURRENT APPLICATION NUMBER: US/10/052,482
PRIORITY FILING DATE: 2002-08-15/07/377
PRIORITY APPLICATION NUMBER: US 09/747,377
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US 09/798,586
PRIORITY FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 241
SOFTWARE: PatentIn version 3.1
SEQ ID NO 223
LENGTH: 79467
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (4095)..(4369)
OTHER INFORMATION: "n" at positions 4099 to 4369 can be any base
FEATURE:
NAME/KEY: misc feature
LOCATION: (5502)..(5521)
OTHER INFORMATION: "n" at positions 5502 to 5521 can be any base
FEATURE:
NAME/KEY: misc feature
LOCATION: (10089)..(10620)
OTHER INFORMATION: "n" at positions 10089 to 10620 can be any base
FEATURE:
NAME/KEY: misc feature
LOCATION: (13273)..(13370)
OTHER INFORMATION: "n" at positions 13273 to 13370 can be any base
FEATURE:
NAME/KEY: misc feature
LOCATION: (20762)..(20781)
OTHER INFORMATION: "n" at positions 20762 to 20781 can be any base
FEATURE:
NAME/KEY: misc feature
LOCATION: (30916)..(30916)
OTHER INFORMATION: "n" at positions 30916 to 30916 can be any base
FEATURE:
NAME/KEY: misc feature
LOCATION: (46772)..(46772)
OTHER INFORMATION: "n" at positions 46759 to 46772 can be any base
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/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (77382)..(77401)
/ OTHER INFORMATION: "n" at positions 77372 to 77401 can be any base
US-10-052-482-223
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Search completed: March 6, 2006, 03:55:15  
Job time : 226.751 secs

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Query Match 19.5%; Score 30.6; DB 7; Length 79467;
Best Local Similarity 56.4%; Pred. No. 39;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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```
OY 51 TTCATCGTCCAGCTTGCCATCTCTGAACCAAGAGTACTCTCCCAACATCCAT 110
Db 53779 TCCACTAGTGTCTCTCTCTGGAACAGCTGTCTAGTCACACACACCA 53838
```

```
OY 111 CTTACTGATGCACTTCCATGCAACACGACATATGTTTC 151
Db 53839 CACACACACACACACACACACACACACACACACAGCTGTGGCTC 53879
```

## RESULT 15

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US-10-317-273-11
/ Sequence 11, Application US/10317273
/ Publication No. US20040110158A1
/ GENERAL INFORMATION:
/ APPLICANT: Kenneth W. Dobie
/ APPLICANT: Tamara Balac Sides
/ TITLE OF INVENTION: MODULATION OF MITOCHONDRIAL RIBOSOMAL PROTEIN L13 EXPRESSION
/ FILE REFERENCE: RTS-0478
/ CURRENT APPLICATION NUMBER: US/10/317,273
/ CURRENT FILING DATE: 2002-12-10
/ NUMBER OF SEQ ID NOS: 159
/ SEQ ID NO 11
/ LENGTH: 52001
/ TYPE: DNA
/ ORGANISM: H. sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 11121, 11122, 11123, 11124, 11125, 11126, 11127, 11128, 11129,
/ LOCATION: 11130, 11131, 11132, 11133, 11134, 11135, 11136, 11137,
/ LOCATION: 11138, 11139, 11140, 11141, 11142, 11143, 11144, 11145,
/ LOCATION: 11146, 11147, 11148, 11149, 11150, 11151, 11152, 11153
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 11154, 11155, 11156, 11157, 11158, 11159, 11160, 11161, 11162,
/ LOCATION: 11163, 11164, 11165, 11166, 11167, 11168, 11169, 11170,
/ LOCATION: 11171, 11172, 11173, 11174, 11175, 11176, 11177, 11178,
/ LOCATION: 11179, 11180, 11181, 11182, 11183, 11184, 11185, 11186
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 11187, 11188, 11189, 11190, 11191, 11192, 11193, 11194, 11195,
/ LOCATION: 11196, 11197, 11198, 11199, 11200, 11201, 11202, 11203,
/ LOCATION: 11204, 11205, 11206, 11207, 11208, 11209, 11210, 11211,
/ LOCATION: 11212, 11213, 11214, 11215, 11216, 11217, 11218, 11219
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 11220
/ OTHER INFORMATION: n = A,T,C or G
US-10-317-273-11
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Query Match 19.4%; Score 30.4; DB 7; Length 52001;
Best Local Similarity 61.2%; Pred. No. 39;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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OY 50 TTCATCGTCCAGCTTGCCATCTCTGAACCAAGAGTACTCTCCCAACATCCA 109
Db 20055 TTTCTTTTCTAAACTGATAATTCATGATAAAGAGATATCAATTTTAAACTACCCA 20114
```

```
OY 110 TCTTACTGATGCAATTGCA 129
Db 20115 TCTTCTCAGCAACTCTCA 20134
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US-09-925-065A-778732/c  
; Sequence 778732, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 778732  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-778732

Query Match 19.6%; Score 30.8; DB 6; Length 601;  
Best Local Similarity 52.3%; Pred. No. 4.3;  
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 12 ACATGGCATCTACATGCTGTTCAACCGTTCGTTCTGTTCCATGTCACGCTTGCT 71  
Db 354 ACATAGTACACTTATTATTATTGTTACTGTTGTCATTAGATATTATACCTTCCT 295  
Qy 72 ATTCTGAACCAAGAGATACCTACTCCCAACATCCATCTTACTGACATCTTCATG 131  
Db 294 ATTATTAATGATTAATTTTCTATACATACATGATTTTCTACCATATTATCTTCTTA 235  
Qy 132 CAACACGCA 141  
Db 234 AACACTGACA 225

## RESULT 3

US-11-117-187-185  
; Sequence 185, Application US/11117187  
; Publication No. US20050266560A1  
; GENERAL INFORMATION:  
; APPLICANT: PREUSS, DAPHNE  
; APPLICANT: COPELHAVER, GREGORY  
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS  
; FILE REFERENCE: ARCD:309US  
; CURRENT FILING DATE: 2005-04-28  
; PRIOR APPLICATION NUMBER: US/09/531,120  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/125,219  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 185  
; LENGTH: 64415  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (9960)..(21146)  
; OTHER INFORMATION: N = A, C G, or T/U  
US-11-117-187-185

Query Match 19.5%; Score 30.6; DB 12; Length 64415;

Best Local Similarity 58.1%; Pred. No. 20;  
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
Qy 65 CTTCGCTATTCTGACCAAGAGATACCTACTCCCAACATCATCTTACTATGCAAC 124  
Db 7117 CTTCCTCTTTAAGTATTATATATATATTTGCTCTCTTAACATTAACCTTACACC 7176  
Qy 125 TTCGATCAAAACGACATATGTTTCTGTAAC 157  
Db 7177 TTAATCCAAACCTTAATCTAATCTTAAAC 7209

## RESULT 4

US-11-121-086-13/c  
; Sequence 13, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13  
; LENGTH: 191797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-13

Query Match 19.4%; Score 30.4; DB 12; Length 191797;  
Best Local Similarity 57.3%; Pred. No. 32;  
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 55 TCGTCAAGCTTGCTATTCTGTAACCAAGAGATACCTACTCCCAACATCATCTTAA 114  
Db 162845 TCCTCAGATCGCTCTATTGTAATATATTAACGCTTACACCAACACATCATATA 162786  
Qy 115 CTCATGCACTTCGATGCAAAACGACATATGTT 150  
Db 162785 TCATTTTACTCCACACACACACATTTT 162750

## RESULT 5

US-09-925-065A-153052  
; Sequence 153052, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 153052  
; LENGTH: 436  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-925-065A-153052

Query Match 19.2%; Score 30.2; DB 6; Length 436;  
Best Local Similarity 60.2%; Pred. No. 6.1;  
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 GTCATCAGATGAGCAATGCTTGTCAACCGTTCGCTTGTTCATGCTCAAG 63  
DB 256 GGCCTCTGCTTGAAGAGCCATGCTTTAAAGCCCTTGTCTTCGCTTGAAT 315

QY 64 CCTGCTATTTGACCAAG 86  
DB 316 TCATGATATTTTGAACAGAG 338

RESULT 5  
US-09-925-065A-285326  
Sequence 285326, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 285326  
LENGTH: 617  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-925-065A-285326

Query Match 19.0%; Score 29.8; DB 6; Length 617;  
Best Local Similarity 60.5%; Pred. No. 9;  
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 74 TCTGAACCAAGAGATCTCTCCAAACATCATCTTACTCATGCAATTCATGCA 133  
DB 373 TGTGTGAATTTATATCACTTCCAAACATCCAGATTGTGACAACTTACTCC 432

QY 134 AACAGCAGATATGTTCTCG 154  
DB 433 TACCTGACCTGAAGTTAATG 453

RESULT 7  
US-09-925-065A-285327  
Sequence 285327, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 285327  
LENGTH: 617  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-925-065A-285327

Query Match 19.0%; Score 29.8; DB 6; Length 617;  
Best Local Similarity 60.5%; Pred. No. 9;  
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 74 TCTGAACCAAGAGATCTCTCCAAACATCATCTTACTCATGCAATTCATGCA 133  
DB 373 TGTGTGAATTTATATCACTTCCAAACATCCAGATTGTGACAACTTACTCC 432

QY 134 AACAGCAGATATGTTCTCG 154  
DB 433 TACCTGACCTGAAGTTAATG 453

RESULT 8  
US-09-925-065A-285328  
Sequence 285328, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 285328  
LENGTH: 617  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-925-065A-285328

Query Match 19.0%; Score 29.8; DB 6; Length 617;  
Best Local Similarity 60.5%; Pred. No. 9;  
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 74 TCTGAACCAAGAGATCTCTCCAAACATCATCTTACTCATGCAATTCATGCA 133  
DB 373 TGTGTGAATTTATATCACTTCCAAACATCCAGATTGTGACAACTTACTCC 432

QY 134 AACAGCAGATATGTTCTCG 154  
DB 433 TACCTGACCTGAAGTTAATG 453

RESULT 9  
US-09-925-065A-12385  
Sequence 12385, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:

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/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12385
/ LENGTH: 1363
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-12385

Query Match          19.0%; Score 29.8; DB 6; Length 1363;
Best Local Similarity 50.3%; Pred. No. 11;
Matches 73; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 6 CATCTACATGACATGATGCTGTTCAACCGTTCCTTGTTCATGTCACAGCC 65
DB 765 CACCGACCTGCGCAAGATGATGATTTCTTAACCATGTCATGCTTCTTCTG 824

QY 66 TTGCTATCTGACACCAAGATACCTACCTCCCAACATCCATCTTACTGACCACT 125
DB 825 TGTGTCTCTGTTGGCATGATGATGACAGAAAAAGATCGCTTATTAATGCACTT 884

QY 126 TCCATGCACACGACGACATATGTTT 150
DB 885 GAGATGGGAAAAATTCAGTACGTGT 909

RESULT 10
US-11-117-187-209/c
/ Sequence 209, Application US/11117187
/ Publication No. US20050266560A1
/ GENERAL INFORMATION:
/ APPLICANT: PREUSS, DAPHNE
/ APPLICANT: COENHAVER, GREGORY
/ TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
/ FILE REFERENCE: ARCD:309US
/ CURRENT APPLICATION NUMBER: US/11/117,187
/ CURRENT FILING DATE: 2005-04-28
/ PRIOR APPLICATION NUMBER: US/09/531,120
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: 60/125,219
/ PRIOR FILING DATE: 1999-03-18
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 209
/ LENGTH: 611587
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-11-117-187-209

Query Match          18.7%; Score 29.4; DB 12; Length 611587;
Best Local Similarity 52.0%; Pred. No. 91;
Matches 66; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
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DB 270084 GCTTGTAGAAAAAACCCCTTCTTCTTATGAATGCTTACTGTCACCTGC 270025
QY 128 CATGCA 134
DB 270024 GATACAA 270018

RESULT 11
US-09-925-065A-805392
/ Sequence 805392, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 805392
/ LENGTH: 544
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-805392

Query Match          18.3%; Score 28.8; DB 6; Length 544;
Best Local Similarity 69.6%; Pred. No. 18;
Matches 39; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 71 TATCTGACCAAGAGATGATCTGCTCCCAACATCATCTTACTGATGCACTT 126
DB 23 TATTAAGAAAAAGAAAAAACCAAAAAACCAAAAAATTCACATTTCCAAATTC 78

RESULT 12
US-10-750-185-47517
/ Sequence 47517, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMT GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR IMPROVING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 47517
/ LENGTH: 1370
/ TYPE: DNA
/ ORGANISM: Bovine
US-10-750-185-47517

Query Match          18.3%; Score 28.8; DB 8; Length 1370;
```

```

Best Local Similarity 54.8%; Pred. No. 24;
Matches 57; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 47 TTGTTCCATGTCGCAACCTTGCCTTCTGTAACCAAGAGATCTCTACTCCCAACAT 106
DB 660 TTGTTCTCATGCTGCGCTCCATTCAGGACTAGAACTTAAATCTCGAATTAAT 719
QY 107 CCATTTACTCATGCACTTCCATGCAACCAACGACATATGTTT 150
DB 720 CTTGTGCAACTAGAAATTTGTGACAGAAATCAAAATATGTTT 763

RESULT 13
US-10-750-623-47517
; Sequence 47517, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: WMI1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47517
; LENGTH: 1370
; TYPE: DNA
; ORGANISM: Bovine 1986680570548
US-10-750-623-47517

Query Match
Best Local Similarity 54.8%; Score 28.8; DB 8; Length 1370;
Matches 57; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 47 TTGTTCCATGTCGCAACCTTGCCTTCTGTAACCAAGAGATCTCTACTCCCAACAT 106
DB 660 TTGTTCTCATGCTGCGCTCCATTCAGGACTAGAACTTAAATCTCGAATTAAT 719
QY 107 CCATTTACTCATGCACTTCCATGCAACCAACGACATATGTTT 150
DB 720 CTTGTGCAACTAGAAATTTGTGACAGAAATCAAAATATGTTT 763

RESULT 14
US-09-925-065A-845392
; Sequence 845392, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 845392
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-845392

Query Match
Best Local Similarity 54.9%; Score 28.4; DB 6; Length 628;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 30 TTGTTCAACGCTTCTGTCATGTCGCAAGCCTTGCCTATTTGAAACCAAGAGAT 89
DB 495 TGGTCTGCTCCAGATAGATGATGTTCTTGAAGACTTGATCAATTTAAAGTGGCGCT 554
QY 90 ACCTACTCCCAACATTCATTTTCTGATGCACTTGCATG 131
DB 555 CCCACTGCCCCACTCTCTCTGCTCTGCTCTTGGCATG 596

RESULT 15
US-09-925-065A-33976/c
; Sequence 33976, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33976
; LENGTH: 1691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-33976

Query Match
Best Local Similarity 54.9%; Score 28.4; DB 6; Length 1691;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 30 TTGTTCAACGCTTCTGTCATGTCGCAAGCCTTGCCTATTTGAAACCAAGAGAT 89
DB 1191 TGGTCTGCTCCAGATAGATGATGTTCTTGAAGACTTGATCAATTTAAAGTGGCGCT 1132
QY 90 ACCTACTCCCAACATTCATTTTCTGATGCACTTGCATG 131
DB 1131 CCCACTGCCCCACTCTCTCTGCTCTGCTCTTGGCATG 1090

Search completed: March 6, 2006, 10:32:51
Job time: 165.89 secs

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CC present sequence represents a DNA fragment -152 to -181 bases upstream of  
CC the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region  
CC nucleotide sequence  
XX  
SQ Sequence 30 BP; 4 A; 9 C; 5 G; 12 T; 0 U; 0 Other;  
Query Match 100.0%; Score 30; DB 5; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.0045;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CATGCTGTTCACCGTTCGTTGTTCCA 30  
DB 1 CATGCTGTTCACCGTTCGTTGTTCCA 30  
RESULT 2  
AAH76340  
ID AAH76340 standard; DNA; 255 BP.  
XX  
AC AAH76340;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Z. mays Ms45 promoter fragment.  
XX  
KM Ms45; male tissue; regulatory region; transcription; male fertility;  
XX hybrid seed; promoter; ds.  
XX  
OS Zea mays.  
XX  
PN WO200160997-A2.  
XX  
PD 23-AUG-2001.  
XX  
PR 13-FEB-2001; 2001WO-US004527.  
XX  
PR 15-FEB-2000; 2000US-00504487.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;  
XX  
DR WPI; 2001-514772/56.  
XX  
PT A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the Ms45 gene useful for  
PT mediating fertility in a male plant.  
XX  
PS Example 5; Fig 8; 50BP; English.  
XX  
CC The invention provides a male tissue-preferred regulatory region (I)  
CC comprising nucleotide sequences essential for initiating transcription of  
CC the Ms45 gene. A method of mediating male fertility in a plant is  
CC provided that involves introducing an expression vector comprising a  
CC promoter operably linked to (I) into a plant where the exogenous gene  
CC impacts male fertility of the plant and (I) controls expression of the  
CC exogenous gene. A method of producing hybrid seeds is also provided. The  
CC present sequence represents a Z. mays Ms45 promoter fragment  
XX  
SQ Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;  
Query Match 100.0%; Score 30; DB 5; Length 255;  
Best Local Similarity 100.0%; Pred. No. 0.0058;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CATGCTGTTCACCGTTCGTTGTTCCA 30  
DB 39 CATGCTGTTCACCGTTCGTTGTTCCA 68  
RESULT 3  
AAH07408  
ID AAH07408 standard; DNA; 1394 BP.

XX  
AC AAH07408;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE Zea mays Ms45 male tissue-preferred regulatory region.  
XX  
KM Ms45; male; tissue-preferred; regulatory region; plant cells;  
XX plant tissue; differentiated; maize; hybrid seed; fertility; ss.  
XX  
OS Zea mays.  
XX  
PN WO9859061-A1.  
XX  
PD 30-DEC-1998.  
XX  
PR 19-JUN-1998; 98WO-US012895.  
XX  
PR 23-JUN-1997; 97US-00880499.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL;  
XX  
DR WPI; 1999-105628/09.  
XX  
PT New nucleic acid encoding a Ms45 male tissue-preferred regulatory region  
PT - useful in mediating plant fertility, especially hybrid seed production.  
XX  
PS Claim 2; Page 22-23; 39pp; English.  
XX  
CC The sequence is that encoding an Ms45 male tissue-preferred regulatory  
CC region. It may be used in the construction of a vector for a method of  
CC producing exogenous genes in a male tissue- preferred manner, which is  
CC useful in restoring or conferring fertility, such as in hybrid seed  
CC production. In conferring fertility, a monocot/dicot plant is transformed  
CC with the exogenous nucleotide sequence (a male sterility gene, preferably  
CC Ms45), which encodes a product selected from auxins, rolB and dipheria  
CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile  
CC and infertile plants  
XX  
SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;  
Query Match 100.0%; Score 30; DB 2; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 0.007;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CATGCTGTTCACCGTTCGTTGTTCCA 30  
DB 1179 CATGCTGTTCACCGTTCGTTGTTCCA 1208  
RESULT 4  
AAH07409  
ID AAH07409 standard; DNA; 1394 BP.  
XX  
AC AAH07409;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE Zea mays Ms45 male tissue-preferred regulatory region.  
XX  
KM Ms45; male; tissue-preferred; regulatory region; plant cells;  
XX plant tissue; differentiated; hybrid seed; fertility; ss.  
XX  
OS Zea mays.  
XX  
PN WO9859061-A1.  
XX  
PD 30-DEC-1998.  
XX  
PR 19-JUN-1998; 98WO-US012895.  
XX

PR 23-JUN-1997; 97US-00880499.  
XX  
XX (PION-) PIONEER HI-BRED INT INC.  
XX  
XX  
PI Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL,  
DR WPI; 1999-105628/09.  
XX  
PT New nucleic acid encoding a Ms45 male tissue-preferred regulatory region  
PT - useful in mediating plant fertility, especially hybrid seed production.  
PS Claim 3; Page 23-24; 39pp; English.  
XX  
XX The sequence is that encoding an Ms45 male tissue-preferred regulatory  
CC region. It may be used in the construction of a vector for a method of  
CC producing exogenous genes in a male tissue-preferred manner, which is  
CC useful in restoring or conferring fertility, such as in hybrid seed  
CC production. In conferring fertility, a monocot/dicot plant is transformed  
CC with the exogenous nucleotide sequence (a male sterility gene, preferably  
CC Ms45), which encodes a product selected from auxins, rolb and dipheria  
CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile  
CC and infertile plants  
XX  
SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;  
Query Match 100.0%; Score 30; DB 2; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 0.007;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CATGCTGTTCACCGCTTGTGTTCCA 30  
DB 1179 CATGCTGTTCACCGCTTGTGTTCCA 1208  
RESULT 5  
AAH76332  
ID AAH76332 standard; DNA; 1394 BP.  
XX  
XX  
AC AAH76332;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.  
XX  
XX Ms45; male tissue; regulatory region; transcription; male fertility;  
XX hybrid seed; ds.  
XX  
XX Zea mays.  
XX  
XX WO200160997-A2.  
XX  
XX 23-AUG-2001.  
XX  
XX 13-FEB-2001; 2001WO-US004527.  
XX  
XX 15-FEB-2000; 2000US-00504487.  
XX  
XX (PION-) PIONEER HI-BRED INT INC.  
XX  
XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;  
XX WPI; 2001-514772/56.  
XX  
XX  
PT A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the Ms45 gene useful for  
PT mediating fertility in a male plant.  
PS Claim 4; Page 46; 50pp; English.  
XX  
XX The invention provides a male tissue-preferred regulatory region (1)  
CC comprising nucleotide sequences essential for initiating transcription of  
CC the Ms45 gene. A method of producing hybrid seeds is also provided. The  
CC Ms45 gene. A method of mediating male fertility in a plant is  
CC provided that involves introducing an expression vector comprising a

CC promoter operably linked to (1) into a plant where the exogenous gene  
CC impacts male fertility of the plant and (1) controls expression of the  
CC exogenous gene. A method of producing hybrid seeds is also provided. The  
CC present sequence represents a nucleic acid sequence encoding an Ms45 male  
CC tissue preferred regulatory region from Z. mays  
XX  
SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;  
Query Match 100.0%; Score 30; DB 5; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 0.007;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CATGCTGTTCACCGCTTGTGTTCCA 30  
DB 1179 CATGCTGTTCACCGCTTGTGTTCCA 1208  
RESULT 6  
AAH76333  
ID AAH76333 standard; DNA; 1394 BP.  
XX  
XX  
AC AAH76333;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.  
XX  
XX Ms45; male tissue; regulatory region; transcription; male fertility;  
XX hybrid seed; ds.  
XX  
XX Zea mays.  
XX  
XX WO200160997-A2.  
XX  
XX 23-AUG-2001.  
XX  
XX 13-FEB-2001; 2001WO-US004527.  
XX  
XX 15-FEB-2000; 2000US-00504487.  
XX  
XX (PION-) PIONEER HI-BRED INT INC.  
XX  
XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;  
XX WPI; 2001-514772/56.  
XX  
XX  
PT A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the Ms45 gene useful for  
PT mediating fertility in a male plant.  
PS Claim 4; Page 47; 50pp; English.  
XX  
XX The invention provides a male tissue-preferred regulatory region (1)  
CC comprising nucleotide sequences essential for initiating transcription of  
CC the Ms45 gene. A method of mediating male fertility in a plant is  
CC provided that involves introducing an expression vector comprising a  
CC promoter operably linked to (1) into a plant where the exogenous gene  
CC impacts male fertility of the plant and (1) controls expression of the  
CC exogenous gene. A method of producing hybrid seeds is also provided. The  
CC present sequence represents a nucleic acid sequence encoding an Ms45 male  
CC tissue preferred regulatory region from Z. mays  
XX  
SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;  
Query Match 100.0%; Score 30; DB 5; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 0.007;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CATGCTGTTCACCGCTTGTGTTCCA 30  
DB 1179 CATGCTGTTCACCGCTTGTGTTCCA 1208

```
RESULT 7
AAH76334
XX AAH76334 standard; DNA; 158 BP.
XX
XX AAH76334;
XX
XX 29-OCT-2001 (first entry)
XX
XX Z. mays Ms45 male tissue-preferred regulatory region fragment.
DE
XX Ms45; male tissue; regulatory region; transcription; male fertility;
XX hybrid seed; ds.
XX
XX Zea mays.
XX
XX WO200160997-A2.
XX
XX 23-AUG-2001.
XX
XX 13-FEB-2001; 2001WO-US004527.
XX
XX 15-FEB-2000; 2000US-00504487.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Albersen MC, Fox TW, Garnat CW, Huffman G, Kendall TL;
XX WPI; 2001-514772/56.
XX
XX A male tissue-preferred regulatory region comprising nucleotide sequences
XX essential for initiating transcription of the MS45 gene useful for
XX mediating fertility in a male plant.
XX
XX Claim 5; Page 47; 50pp; English.
XX
XX The invention provides a male tissue-preferred regulatory region (I)
XX comprising nucleotide sequences essential for initiating transcription of
XX the MS45 gene. A method of mediating male fertility in a plant is
XX provided that involves introducing an expression vector comprising a
XX promoter operably linked to (I) into a plant where the exogenous gene
XX impacts male fertility of the plant and (I) controls expression of the
XX exogenous gene. A method of producing hybrid seeds is also provided. The
XX present sequence represents a DNA fragment -38 to -195 bases upstream of
XX the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
XX nucleotide sequence
XX
XX Sequence 158 BP; 41 A; 50 C; 21 G; 46 T; 0 U; 0 Other;
SQ
Query Match 80.7%; Score 24.2; DB 5; Length 158;
Best Local Similarity 89.7%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CATGCTGTTCACCGCTTCCTTGTTC 29
| | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | |
DB 25 CATGCTGTTCACCGCTTCCTTGTTC 53
| | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | |
RESULT 8
ABO75351/C
ID ABO75351 standard; CDNA; 1304 BP.
XX
XX ABO75351;
XX
XX 05-NOV-2002 (first entry)
XX
XX Human lung specific nucleic acid sequence SEQ ID NO:90.
XX
XX Human lung specific nucleic acid; LSNA; lung specific protein;
XX LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer;
XX squamous cell carcinoma; gene; ss.
XX
XX Homo sapiens.
XX
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PN WO200264788-A2.
XX
XX 22-AUG-2002.
XX
XX 20-NOV-2001; 2001WO-US045080.
XX
XX 20-NOV-2000; 2000US-0252054P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX WPI; 2002-657601/70.
XX
XX New lung specific nucleic acid useful in gene therapy or as vaccines for
XX treating lung cancer (e.g. squamous cell carcinoma) or non-cancerous lung
XX diseases, as well as for diagnosing, monitoring or staging these
XX diseases.
XX
XX Claim 1; Page 206; 282pp; English.
XX
XX The present invention describes an isolated lung specific nucleic acid
XX (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid
XX sequences comprising 17 - 733 amino acids, given in ABB52873 to ABB52965;
XX (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp),
XX given in ABO75262 to ABO75376; (c) selectively hybridizes to (a) or (b);
XX or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific
XX protein (LSP) sequences have cytostatic activity and can be used in gene
XX therapy and vaccines. LSNA and LSPs are useful for diagnosing and
XX monitoring the presence and metastases of lung cancer in a patient. An
XX antibody that specifically binds to an LSP can be used for determining
XX the presence of an LSP in a sample, as well as for treating a patient
XX with lung cancer, particularly by inducing an immune response against the
XX lung cancer cell expressing the LSNA or LSPs. In particular, these LSNA
XX and LSPs are useful for identifying, diagnosing, monitoring, staging,
XX imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-
XX cancerous disease states in lung
XX
XX Sequence 1304 BP; 352 A; 347 C; 314 G; 291 T; 0 U; 0 Other;
SQ
Query Match 73.3%; Score 22; DB 6; Length 1304;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 CATGCTGTTCACCGCTTCCTTGTTC 30
| | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | |
DB 1155 CTTCCTGTTCACCGCTTCCTTGTTC 1126
| | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | |
RESULT 9
AB213819
ID AB213819 standard; DNA; 1542 BP.
XX
XX AB213819;
XX
XX 21-JAN-2003 (first entry)
XX
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 1624.
XX
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
XX Arabidopsis thaliana.
XX
XX WO200216655-A2.
XX
XX 28-FEB-2002.
XX
XX 24-AUG-2001; 2001WO-US026685.
XX
XX 24-AUG-2000; 2000US-0227866P.
XX
XX 26-JAN-2001; 2001US-0264647P.
XX
XX 22-JUN-2001; 2001US-0300111P.
XX
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PA (SCN1) SCRIpps RES INST.  
 PA (SYGN) STINGENT PARTICIPATIONS AG.  
 XX Harper JF, Kreps J, Wang X, Zhu T;  
 XX WPI; 2002-304127/34.  
 DR  
 PT Identifying a stress condition to which a plant cell has been exposed and  
 PT producing plants with increased tolerance to these abiotic stresses.  
 PS Claim 14; SEQ ID NO 1624; 577bp + Sequence Listing; English.  
 XX  
 CC The invention relates to identifying a stress condition to which a plant  
 CC cell has been exposed, comprising: (a) contacting nucleic acid  
 CC representative of expressed polynucleotides in the plant cell with an  
 CC array or probes representative of the plant cell genome; and (b)  
 CC detecting a profile of expressed polynucleotides in the plant cell  
 CC characteristic of a stress response. The method is useful in the  
 CC production of transgenic plants, cells and seeds and in producing plants  
 CC with increased tolerance to abiotic stress. The present sequence is that  
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used  
 CC in methods of the invention. Note: The sequence data for this patent is  
 CC not represented in the printed specification but is based on sequence  
 CC information supplied to Derwent by the European Patent Office  
 XX  
 SQ Sequence 1542 BP; 345 A; 382 C; 370 G; 445 T; 0 U; 0 Other;  
 Query Match 68.0%; Score 20.4; DB 6; Length 1542;  
 Best Local Similarity 80.0%; Pred. No. 91;  
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 CAGCGTGTTCACCGCTTCGCTTCA 30  
 DB 237 CAGCGTGTTCACCAACGTCGCTTCA 266  
 RESULT 10  
 ID ACA44013 standard; DNA; 2397 BP.  
 XX ACA44013;  
 AC  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Prokaryotic essential gene #25670.  
 XX  
 KW Antisense, ds; prokaryotic essential gene; cell proliferation;  
 KW drug design; gene.  
 XX  
 OS Pseudomonas putida.  
 XX  
 FN W0200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002MO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 XX  
 PR 06-SEP-2001; 2001US-00948993.  
 XX  
 PR 25-OCT-2001; 2001US-0342923P.  
 XX  
 PR 08-FEB-2002; 2002US-00072851.  
 XX  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HR;  
 XX WPI; 2003-029926/02.  
 DR P-FSDB; AB040143.  
 DR  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 14; SEQ ID NO 31883; 1766bp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway;  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation; (9)  
 CC pathway in which a proliferation-regulated gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the gene  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
 CC prokaryotic essential genes. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 2397 BP; 415 A; 825 C; 781 G; 376 T; 0 U; 0 Other;  
 Query Match 67.3%; Score 20.2; DB 8; Length 2397;  
 Best Local Similarity 88.0%; Pred. No. 1.2e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CAGCGTGTTCACCGCTTCGCTTG 25  
 DB 516 CAGCGTGTTCACCGCTTCGCTTG 540  
 RESULT 11  
 ID ACL37526 standard; cDNA; 2000 BP.  
 XX ACL37526;  
 AC  
 DT 02-JUN-2005 (first entry)  
 XX  
 DE Rice stress-regulated promoter SEQ ID NO:16089.  
 XX  
 KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;  
 KW agriculture.  
 XX  
 OS Oryza sativa.  
 XX  
 FN W02003008540-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002MO-US019668.  
 XX  
 PR 22-JUN-2001; 2001US-0300112P.  
 XX  
 PR 24-AUG-2001; 2001US-0314662P.  
 XX  
 PR 26-SEP-2001; 2001US-0325277P.  
 XX  
 PR 21-NOV-2001; 2001US-0332132P.  
 XX

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Krieps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;  
PI Moughamer T, Provart N, Ricke D, Zhu T;  
XX  
DR WPI; 2003-248011/24.  
XX  
PT New stress-responsive nucleic acid, useful for altering the  
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
PT stress, salt stress or osmotic stress.  
XX  
PS Claim 48; SEQ ID NO 16089; 89pp; English.  
XX  
CC The invention relates to novel abiotic stress responsive polynucleotides  
CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
CC cells, and plants containing such polynucleotides. Also disclosed are  
CC methods for using the polynucleotides and polypeptides to alter the  
CC responsiveness of a plant to abiotic stress. The invention is useful in  
CC agriculture. The nucleic acid is useful for determining whether a test  
CC plant has been exposed to an abiotic stress condition. It is also useful  
CC for selecting an agent that alters abiotic stress regulated  
CC polynucleotide expression in a plant cell, and to identify a homolog or  
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
CC molecule and the polypeptide encoded by it are useful in altering the  
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
CC stress, osmotic stress or any of their combinations. The present sequence  
CC is used in the exemplification of the invention  
XX  
SQ Sequence 2000 BP; 607 A; 443 C; 399 G; 549 T; 0 U; 2 Other;  
Query Match 66.7%; Score 20; DB 11; Length 2000;  
Best Local Similarity 82.1%; Pred. No. 1.4e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Oy 3 TGCTTGTTCACCGTTCGCTTGTTCCTCA 30  
Db 1576 TGCATGTTTACCGTTCGCTTATTCGA 1603  
RESULT 12  
ID ACL34976  
XX ACL34976 standard; cDNA; 2000 BP.  
XX  
AC ACL34976;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE Rice stress-regulated promoter SEQ ID NO:13539.  
XX  
DE ss; abiotic stress tolerance; transgenic plant; plant; cereal;  
KM agriculture.  
XX  
OS Oryza sativa.  
XX  
PN MO2003008540-A2.  
XX  
PD 30-JAN-2003.  
XX  
PF 21-JUN-2002; 2002MO-US019668.  
XX  
PR 22-JUN-2001; 2001US-0300112P.  
PR 24-AUG-2001; 2001US-0314662P.  
PR 26-SEP-2001; 2001US-0328277P.  
PR 21-NOV-2001; 2001US-0332132P.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Krieps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;  
PI Moughamer T, Provart N, Ricke D, Zhu T;  
XX  
DR WPI; 2003-248011/24.  
XX  
PT New stress-responsive nucleic acid, useful for altering the

PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
PT stress, salt stress or osmotic stress.  
XX  
PS Claim 48; SEQ ID NO 13539; 89pp; English.  
XX  
CC The invention relates to novel abiotic stress responsive polynucleotides  
CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
CC cells, and plants containing such polynucleotides. Also disclosed are  
CC methods for using the polynucleotides and polypeptides to alter the  
CC responsiveness of a plant to abiotic stress. The invention is useful in  
CC agriculture. The nucleic acid is useful for determining whether a test  
CC plant has been exposed to an abiotic stress condition. It is also useful  
CC for selecting an agent that alters abiotic stress regulated  
CC polynucleotide expression in a plant cell, and to identify a homolog or  
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
CC molecule and the polypeptide encoded by it are useful in altering the  
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
CC stress, osmotic stress or any of their combinations. The present sequence  
CC is used in the exemplification of the invention  
XX  
SQ Sequence 2000 BP; 552 A; 438 C; 444 G; 566 T; 0 U; 0 Other;  
Query Match 66.7%; Score 20; DB 11; Length 2000;  
Best Local Similarity 82.1%; Pred. No. 1.4e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Oy 3 TGCTTGTTCACCGTTCGCTTGTTCCTCA 30  
Db 1179 TACATGTTTACCGTTCGCTTATTCGA 1206  
RESULT 13  
ID ADJ40785  
XX ADJ40785 standard; cDNA; 2000 BP.  
XX  
AC ADJ40785;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Plant cDNA #1785.  
XX  
KM Plant; gene; ss; transcription; plant genome augmentation; cereal;  
KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;  
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;  
KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;  
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;  
KM antifungal.  
XX  
OS Eukaryota.  
XX  
PN US2004016025-A1.  
XX  
PD 22-JAN-2004.  
XX  
PF 26-SEP-2002; 2002US-00260238.  
XX  
PR 26-SEP-2001; 2001US-0325277P.  
PR 26-SEP-2001; 2001US-0325448P.  
PR 04-APR-2002; 2002US-0370620P.  
XX  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KRIEPS J.  
PA (PROV/) PROVART N.  
PA (RICKE/) RICKE D.  
PA (ZHUT/) ZHU T.  
XX  
PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;

PI Goff SA, Katagiri F, Kreps J, Provart N, Rieke D, Zhu T;  
XX  
DR WPI; 2004-190374/18.  
XX  
PT New rice promoter, useful for manipulating crop plants to alter or  
XX improve phenotypic characteristics, e.g. produce large quantities of oil  
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance  
XX or high nutritional value.  
XX  
PS Claim 26; SEQ ID NO 1785; 230bp; English.  
XX  
CC The invention relates to plant nucleotide sequences that direct seed,  
CC leaf, and/or stem, panicle, root- or pollen-specific or -preferential  
CC or constitutive transcription of an operatively linked nucleic acid  
CC segment. The invention also relates to a method for augmenting a plant  
CC genome and a method of identifying a gene, where its expression is  
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive  
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,  
CC sorghum, cotton, peanut, tobacco or sugar beet, preferably maize, barley,  
CC encode are useful for manipulating crop plants to alter or improve  
CC phenotypic characteristics, to produce large quantities of oil or  
CC proteins, to incur resistance to insecticides, viruses or fungi, and to  
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants  
CC have a high nutritional value with reduced apical dominance or dwarfism,  
CC early flowering or altered metabolic pathways. This sequence represents a  
CC plant nucleic acid of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification but was obtained in  
CC electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 2000 BP; 552 A; 438 C; 444 G; 566 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 20; DB 12; Length 2000;  
Best Local Similarity 82.1%; Pred. No. 1.4e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
XX  
QY 3 TGGCTTCAACCGTTCCTCTTCA 30  
DB 1179 TACATGTTTACCGTTCCTCTTCA 1206  
XX  
RESULT 14  
AC135519 standard; cDNA; 1735 BP.  
XX  
AC AC135519;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE Rice stress-regulated promoter SEQ ID NO:14082.  
XX  
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;  
XX agriculture.  
XX  
OS Oryza sativa.  
XX  
PN WO2003008540-A2.  
XX  
PD 30-JAN-2003.  
XX  
PF 21-JUN-2002; 2002WO-US019666.  
XX  
PR 22-JUN-2001; 2001US-0300113P.  
XX 24-AUG-2001; 2001US-0314663P.  
XX 26-SEP-2001; 2001US-0325377P.  
XX 21-NOV-2001; 2001US-0332133P.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,  
PI Moughamer T, Provart N, Rieke D, Zhu T;  
XX WPI; 2003-248011/24.  
DR

XX  
PT New stress-responsive nucleic acid, useful for altering the  
XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
XX stress, salt stress or osmotic stress.  
XX  
PS Claim 48; SEQ ID NO 14082; 89bp; English.  
XX  
CC The invention relates to novel abiotic stress responsive polynucleotides  
CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
CC cells, and plants containing such polynucleotides. Also disclosed are  
CC methods for using the polynucleotides and polypeptides to alter the  
CC responsiveness of a plant to abiotic stress. The invention is useful in  
CC agriculture. The nucleic acid is useful for determining whether a test  
CC plant has been exposed to an abiotic stress condition. It is also useful  
CC for selecting an agent that alters abiotic stress regulated  
CC polynucleotide expression in a plant cell, and to identify a homolog or  
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
CC molecule and the polypeptide encoded by it are useful in altering the  
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
CC stress, osmotic stress or any of their combinations. The present sequence  
CC is used in the exemplification of the invention.  
XX  
SQ Sequence 1735 BP; 502 A; 368 C; 279 G; 581 T; 0 U; 5 Other;  
XX  
Query Match 65.3%; Score 19.6; DB 11; Length 1735;  
Best Local Similarity 84.6%; Pred. No. 2e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 5 CTGTTCAACCGTTCCTCTTCA 30  
DB 394 CAGTTTACCGTTCCTCTTCA 419  
XX  
RESULT 15  
ADA72061 standard; DNA; 2000 BP.  
XX  
AC ADA72061;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice gene, SEQ ID 5386.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; rice;  
XX gene; de.  
XX  
OS Oryza sativa.  
XX  
PN WO2003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
XX 22-JUN-2001; 2001WO-IB001105.  
XX  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX WPI; 2003-175290/17.  
XX  
DR  
XX  
PT Identifying at least one gene involved in plant resistance or response to  
XX pathogenic infection for conferring resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection by determining or detecting plant  
XX gene expression.  
XX  
PS Claim 27; SEQ ID NO 5386; 899bp; English.  
XX  
CC The present invention relates to a method (M1) for identifying genes  
XX involved in plant resistance or response to pathogenic infection. M1  
XX comprises identifying a gene whose expression is significantly altered in

CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.

XX  
SQ Sequence 2000 BP; 605 A; 377 C; 326 G; 690 T; 0 U; 2 Other;

Query Match 65.3%; Score 19.6; DB 8; Length 2000;

Best Local Similarity 84.6%; Pred. No. 2.1e+02;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CTGTGACCGCTGCTTGTCCA 30

DB 974 CATGTTAACCGCTGCTTATCA 999

Search completed: March 5, 2006, 18:11:42  
Job time : 19.9642 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 18:11:59 ; Search time 141.632 Seconds  
(without alignments)  
9910.279 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1179\_1208

Sequence: 1 catgcttgcacacgcgttcgttcga 30

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 segs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: gb\_esi1.\*  
2: gb\_esi2.\*  
3: gb\_esi3.\*  
4: gb\_hic.\*  
5: gb\_esi4.\*  
6: gb\_esi5.\*  
7: gb\_esi6.\*  
8: gb\_esi7.\*  
9: gb\_esi8.\*  
10: gb\_esi9.\*  
11: gb\_esi10.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
C 1	30	100.0	687	9	CC656939
2	30	100.0	915	10	CG224225
3	30	100.0	963	9	CC656933
4	27.4	91.3	296	10	CM445575
5	22.2	74.0	308	10	CG700474
6	21.2	70.7	534	5	BU035739
7	21.2	70.7	626	5	BU030489
8	21.2	70.7	792	7	CN137013
9	21	70.0	154	1	AA811551
C 10	21	70.0	571	11	CR192459
C 11	21	70.0	571	11	CR064270
C 12	21	70.0	599	11	CR233864
C 13	21	70.0	769	11	CR188179
C 14	21	70.0	832	9	CC848693
C 15	21	70.0	835	9	CC860012
16	20.8	69.3	586	7	CO853973
17	20.6	68.7	412	8	R12648
18	20.6	68.7	450	8	R12618
C 19	20.6	68.7	582	1	AU290776
C 20	20.6	68.7	594	8	DR437963
21	20.6	68.7	681	9	AZ817790
C 22	20.6	68.7	1144	9	CC271930

23	20.4	68.0	353	9	A0261553
24	20.4	68.0	373	3	BP857382
25	20.4	68.0	396	2	BE522930
26	20.4	68.0	398	3	BP836596
27	20.4	68.0	514	2	BP354154
28	20.4	68.0	515	3	BP561510
29	20.4	68.0	536	1	AV439701
30	20.4	68.0	559	1	AV825937
C 31	20.4	68.0	560	6	CA230882
C 32	20.4	68.0	590	7	CV153842
C 33	20.4	68.0	598	10	CM788317
C 34	20.4	68.0	600	9	BM76120
C 35	20.4	68.0	602	10	CM583422
36	20.4	68.0	603	9	BZ694195
37	20.4	68.0	615	9	AQ453944
C 38	20.4	68.0	639	7	CV153844
39	20.4	68.0	668	9	AQ260121
40	20.4	68.0	779	6	CD825116
41	20.4	68.0	807	6	CD836362
C 42	20.4	68.0	836	9	BM480110
C 43	20.4	68.0	967	9	BZ684538
C 44	20.4	68.0	1205	9	B10570
C 45	20.2	67.3	431	8	R32995

#### ALIGNMENTS

RESULT 1  
CC656939 687 bp DNA linear GSS 19-JUN-2003  
LOCUS  
DEFINITION OGMDO20TV ZM.0.7.1.5\_KB Zee maye genomic clone ZM8M80554D15,  
genomic survey sequence.  
ACCESSION  
CC656939  
VERSION  
CC656939.1 GI:32060231  
KEYWORDS  
GSS.  
SOURCE  
Zee maye  
ORGANISM  
Zee maye  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 687)

REFERENCE  
AUTHORS  
White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Remick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunez, A., Robbins, D., and Lakey, N.  
TITLE  
JOURNAL  
Unpublished (2002)  
COMMENT  
Other GSSs: OGMDO20TV  
Contact: Cathy White

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208

Email: whitec@tigr.org

Seq primer: TP

Class: methylation filtered.

#### FEATURES

source  
1..687  
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methylation filtered genomic DNA library"

#### ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CATGCTTGCACACGTCGTCGTCGTCGA 30

Db 397 CATGCTGTTCACCGTTCGTTGTTCCA 368

RESULT 2  
LOCUS CG224225 915 bp DNA linear GSS 22-AUG-2003  
DEFINITION OGIAG08TV ZM 0.7 1.5 KB zea maye genomic clone ZMMBMA0716B15,  
genomic survey sequence.

ACCESSION CG224225  
VERSION CG224225  
KEYWORDS GSS,  
SOURCE Zea maye  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 915)  
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T.,  
Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGIAG08TV  
Contact: Cathy WhiteLaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@cigr.org  
Seq primer: TR  
Class: methylation filtered.  
Location/Qualifiers  
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methylation filtered genomic DNA library"

FEATURES  
source

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.026; Mismatches 0; Indels 0; Gaps 0;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACCGTTCGTTGTTCCA 30  
558 CATGCTGTTCACCGTTCGTTGTTCCA 587

Db 558 CATGCTGTTCACCGTTCGTTGTTCCA 587

RESULT 3  
LOCUS CC656933 963 bp DNA linear GSS 19-JUN-2003  
DEFINITION OGMDQ20TM ZM 0.7 1.5 KB zea maye genomic clone ZMMBMA0554D15,  
genomic survey sequence.

ACCESSION CC656933  
VERSION CC656933  
KEYWORDS GSS,  
SOURCE Zea maye  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 963)  
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T.,  
Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGMDQ20TV

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Contact: Cathy WhiteLaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@cigr.org  
Seq primer: TR  
Class: methylation filtered.  
Location/Qualifiers  
1..963  
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/strain="B73"  
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/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

FEATURES  
source

ORIGIN  
Query Match 100.0%; Score 30; DB 9; Length 963;  
Best Local Similarity 100.0%; Pred. No. 0.026; Mismatches 0; Indels 0; Gaps 0;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACCGTTCGTTGTTCCA 30  
776 CATGCTGTTCACCGTTCGTTGTTCCA 805

Db 776 CATGCTGTTCACCGTTCGTTGTTCCA 805

RESULT 4  
LOCUS CW445575 296 bp DNA linear GSS 02-NOV-2004  
DEFINITION feb0001f170m16K Sorghum methylation filtered library (libid: 104)  
Sorghum bicolor genomic clone feb0001f170m16, genomic survey  
sequence.

ACCESSION CW445575  
VERSION CW445575  
KEYWORDS GSS,  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 296)  
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,  
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,  
McKenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korfi,I.F.,  
Rabinowicz,P.D., Lakey,N., McCombie,M.R., Jeddelen,J.A. and  
Martiniussen,R.A.  
Sorghum genome sequencing by methylation filtration  
PLoS Biol. 3 (1), e13 (2005)  
15660154  
Contact: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@origenomics.com  
Plate: feb0001f170 row: m column: 16  
Seq primer: k Reverse  
Class: methylation filtered  
High quality sequence stop: 296.  
Location/Qualifiers  
1..296  
/organism="Sorghum bicolor"  
/mol\_type="genomic DNA"  
/cultivar="Atr623"  
/db\_xref="taxon:4558"  
/clone="feb0001f170m16"  
/clone\_lib="Sorghum methylation filtered library (libid:  
104)"  
/note="Organ: leaf, Vector: pBCSK(-); Site 1: HincII; DNA  
prepped from purified nuclei was randomly sheared."

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pGSK(-) vector and electroporated into *E. coli* cells. This is a methylation filtered library."

## ORIGIN

Query Match 91.3%; Score 27.4; DB 10; Length 296;  
Best Local Similarity 96.6%; Pred. No. 0.3;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATGCTTGTTCACCGCTTCGCTTGTTCAC 30  
DB 140 ATGCTTGTTCACCGCTTCGCTTGTTCACCA 168

RESULT 5  
CG700474 308 bp DNA linear GSS 15-OCT-2003  
LOCUS ZMMBC0174H15f ZMMBC (BcORI) Zea mays genomic clone ZMMBC0174H15  
DEFINITION 5', genomic survey sequence.  
ACCESSION CG700474  
VERSION CG700474.1 GI:37688275  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Bakeryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 308)  
AUTHORS Bharti,A.K., Young,S., Kaychok,S., Keizer,G., Bronzino,A.C., Zohover,V., Fuks,G., Yu,Y., Wang,R. and Messing,D.  
TITLE Sequencing of the maize genome at PGIR (2003c)  
JOURNAL Unpublished (2003)  
COMMENT Contact: Bharti,A.K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: T7  
Class: BAC ends  
High quality sequence start: 57.  
Location/Qualifiers  
1..308  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBC0174H15"  
/lab\_host="E. coli DH10B"  
/clone\_lib="ZMMBC (BcORI)"  
/note="Vector: pTARBAC2.1; Site\_1: BcORI; Site\_2: BcORI"

## FEATURES

ORIGIN  
Query Match 74.0%; Score 22.2; DB 10; Length 308;  
Best Local Similarity 88.9%; Pred. No. 60;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATGCTTGTTCACCGCTTCGCTTGT 27  
DB 226 CATGCTTGTTCACCGCTTCGCTTGT 200

RESULT 6  
BU035739 534 bp mRNA linear EST 23-AUG-2002  
LOCUS BU035739  
DEFINITION OHJ1N19.yg.ab1 OH EFGH sunflower RHA280 Helianthus annuus cDNA  
ACCESSION BU035739  
VERSION BU035739.1 GI:22471259  
KEYWORDS EST.

SOURCE Helianthus annuus (common sunflower)

## ORGANISM

Helianthus annuus  
Bakeryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.  
1 (bases 1 to 534)

## REFERENCE

AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevallier,P., Ziegler,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.  
TITLE Lettuce and Sunflower ESTs from the Composite Genome Project  
JOURNAL http://compogenomics.ucdavis.edu/  
Unpublished (2002)  
CONTACT: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Aamundson Hall, UCD Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmore@ucdavis.edu]  
belongs to contig OH\_Ca\_contig3046, see http://cgpdb.ucdavis.edu/ for details.  
Plate: OHJ7 row: N column: 19.  
Location/Qualifiers  
1..534  
/organism="Helianthus annuus"  
/mol\_type="mRNA"  
/cultivar="RHA280"  
/db\_xref="taxon:4232"  
/clone="OHJ7N19"  
/lab\_host="E. coli"

## FEATURES

ORIGIN  
Query Match 70.7%; Score 21.2; DB 5; Length 534;  
Best Local Similarity 88.5%; Pred. No. 1.8e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGCTTGTTCACCGCTTCGCTTGT 27  
DB 104 ATGCTTGTTCACCGCTTCGCTTGT 79

RESULT 7  
BU030489 626 bp mRNA linear EST 23-AUG-2002  
LOCUS BU030489  
DEFINITION OHJ15120.yg.ab1 OH EFGH sunflower RHA280 Helianthus annuus cDNA  
ACCESSION BU030489  
VERSION BU030489.1 GI:22466009  
KEYWORDS EST.  
SOURCE Helianthus annuus (common sunflower)  
ORGANISM Helianthus annuus  
Bakeryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.  
REFERENCE 1 (bases 1 to 626)  
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevaller,P., Ziegler,J.,

**TITLE**  
Ellison, P., Kolkman, J., Stabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lecture and Sunflower ESTs from the Compositae Genome Project  
<http://compositae.ucdavis.edu/>  
Unpublished (2002)

**JOURNAL**  
Contact: Alexander Kozik (R.W.Michelmore)  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Aamundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: [akozik@ucdavis.edu](mailto:akozik@ucdavis.edu) [[michelmore@ucdavis.edu](mailto:michelmore@ucdavis.edu)]  
belongs to contig OH\_Ca\_Contig3046, see <http://cgdb.ucdavis.edu/>  
for details.  
Plate: OH15 row: 1 column: 20.

**FEATURES**  
source  
Location/Qualifiers

```
1..626
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="RHA280"
/db_xref="taxon:4232"
/clone="QHJ15120"
/lab_host="E.coli"
/clone_1lb="QH_EFGHU sunflower RHA280"
/notes="Vector: pBRCDNA51AB; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB=QH_EFGHU sunflower RHA280
TAG_SEQ=CGAATCGCGG
```

**ORIGIN**  
Query Match 70.7%; Score 21.2; DB 5; Length 626;  
Best Local Similarity 88.5%; Pred. No. 1.9e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy**  
2 ATGCTTGTTCACCGTTCGCTCTTGT 27  
|||||  
Db 104 ATGCTTGTTCACCGTTCGCTCTTGT 79

**RESULT 8**  
CN137013 792 bp mRNA linear EST 01-APR-2004  
LOCUS OX1\_54\_E01\_A002 Oxidatively-stressed leaves and roots Sorghum  
DEFINITION bicolor cDNA clone OX1\_54\_E01\_A002 5', mRNA sequence.  
VERSION CN137013  
KEYWORDS

**ACCESSION**  
CN137013.1 GI:45970259  
EST.  
Sorghum bicolor (sorghum)  
Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.

**REFERENCE**  
AUTHORS 1 (bases 1 to 792)  
Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.  
An EST database from Sorghum: oxidatively stressed leaves and roots  
Unpublished (2003)  
Other ESTs: OX1\_54\_E01\_b1\_A002  
Contact: Cordanier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: [mmpratt@uga.edu](mailto:mmpratt@uga.edu)

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
the Human Genome Center, University of Tokyo Institute of Medical  
Science; plant material and RNA prepared at Texas A & M University;  
sequencing done in the Laboratory for Genomics and Bioinformatics,  
University of Georgia. Sequence ends have been trimmed to exclude  
vector and regions below phred quality 16. Three-prime sequences  
are presented as their reverse complement and have been trimmed to  
exclude polyA.  
Seq primer: Sug5 (CTTCTGCTTAAAGCTGCG).

**FEATURES**  
source  
Location/Qualifiers

```
1..792
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="B7x623"
/db_xref="taxon:4558"
/clone="OX1_54_E01_A002"
/lab_host="DH10B-TI phage-resistant E. coli"
/clone_1lb="Oxidatively-stressed leaves and roots"
/notes="Organ: Leaf and Root; Vector: pMB18-F13; Site_1:  
XhoI; Site_2: XhoI; The library was prepared from polyA+  
RNA from oxidatively stressed, hydroponically grown  
sorghum seedlings. At 8 days of age, growth medium was  
supplemented with hydrogen peroxide to 0.003% and leaves  
were misted with 10 uM methyl viologen. Leaves and roots  
were harvested at 3, 12 and 27 hr after treatment and all  
tissue pooled. Double-stranded cDNA was cloned  
unidirectionally into different DraIII sites of the  
pMB18-F13 vector (5-prime DraIII site is CACTGTGG,  
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA  
insert."
```

**ORIGIN**  
Query Match 70.7%; Score 21.2; DB 7; Length 792;  
Best Local Similarity 88.5%; Pred. No. 1.9e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy**  
5 CTCTTCACCGTTCGCTCTTCCA 30  
|||||  
Db 17 CTCTTCACCGTTCGCTCTTCCA 42

**RESULT 9**  
AA811551/c 154 bp mRNA linear EST 19-FEB-1998  
LOCUS o699e03.81 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1320412 3'  
DEFINITION similar to SW:COPE\_BOVIN Q28104 COATOMER EPSILON SUBUNIT, mRNA  
sequence.  
VERSION AA811551  
KEYWORDS

**ACCESSION**  
AA811551 GI:2881162  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.

**REFERENCE**  
AUTHORS 1 (bases 1 to 154)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-rt@mail.nih.gov](mailto:cgaps-rt@mail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonafio, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www-bio.1nl.gov/btrp/image/image.html](http://www-bio.1nl.gov/btrp/image/image.html)

Trace considered overall poor quality

Insert Length: 1232 Std Error: 0.00  
Seq primer: -40m13 fwd. RT from Amersham  
High quality sequence scop: 1.

## FEATURES

source

1..154  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1320412"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_1ib="NCI CGAP GCB1"  
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I, Site 2: Eco RI, 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, 19D-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - c190(dT) primer  
15'-TGTTACCAATCTGAAGTGGACGCGCCCTCATTTTCTTTTCTTT-3'  
(Pharmacia), digested with Not I and Eco RI adaptors. Library and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 70.0%; Score 21; DB 1; Length 154;  
Best Local Similarity 82.8%; Pred. No. 1.8e+02;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCTGTTCACCGTTCGTTCTGTTCCTCA 30  
Db 43 AACCTGTTCACCGTTCGTTCTGTTCCTCA 15

RESULT 10  
CR192459/c 351 bp DNA linear GSS 06-JUL-2004  
LOCUS Reverse strand read from insert in 5'HPRT insertion targeting and  
DEFINITION chromosome engineering clone MHPN146506, genomic survey sequence.  
ACCESSION CR192459.1 GI:499711308  
VERSION GSS; genome survey sequence; MLCR.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus

## REFERENCE

AUTHORS

Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
Rogers,J. and Bradley,A.

## TITLE

JOURNAL

Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICR

## FEATURES

source

1..351  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN146506"  
/clone\_1ib="MHPN"

## ORIGIN

Query Match 70.0%; Score 21; DB 11; Length 351;  
Best Local Similarity 82.8%; Pred. No. 2.1e+02;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCTGTTCACCGTTCGTTCTGTTCCTCA 30  
Db 307 ATGCTGTTCACCGTTCGTTCTGTTCCTCA 279

RESULT 11  
CR064270/c 571 bp DNA linear GSS 05-JUL-2004  
LOCUS Reverse strand read from insert in 5'HPRT insertion targeting and  
DEFINITION chromosome engineering clone MHPN190119, genomic survey sequence.  
ACCESSION CR064270.1 GI:497977742  
VERSION GSS; genome survey sequence; MLCR.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus

## ORIGIN

source

1..571  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN190119"  
/clone\_1ib="MHPN"

## ORIGIN

Query Match 70.0%; Score 21; DB 11; Length 571;  
Best Local Similarity 82.8%; Pred. No. 2.2e+02;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCTGTTCACCGTTCGTTCTGTTCCTCA 30  
Db 309 ATGCTGTTCACCGTTCGTTCTGTTCCTCA 281

RESULT 12  
CR233964/c 599 bp DNA linear GSS 06-JUL-2004  
LOCUS Reverse strand read from insert in 5'HPRT insertion targeting and  
DEFINITION chromosome engineering clone MHPN144h08, genomic survey sequence.  
ACCESSION CR233964.1 GI:50012813  
VERSION GSS; genome survey sequence; MLCR.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus

## REFERENCE

AUTHORS

Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
Rogers,J. and Bradley,A.

## TITLE

JOURNAL

Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICR

## FEATURES

source

1..599  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN144h08"  
/clone\_1ib="MHPN"

## ORIGIN

Query Match 70.0%; Score 21; DB 11; Length 599;  
Best Local Similarity 82.8%; Pred. No. 2.3e+02;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCTGTTCACCGTTCGTTCTGTTCCTCA 30

```

Db      310 ATCGTGTCCAGCCGTCGTGATGATTCGA 282
|||||
RESULT 13
LOCUS   CRI88179/c
DEFINITION
Reverse strand read from insert in 5'Hprt insertion targeting and
chromosome engineering clone MHPN234h03, genomic survey sequence.
ACCESSION
CRI88179
VERSION  CRI88179.1 GI:49967028
KEYWORDS
GSS: genome survey sequence; MICER.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 769)
  Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
  Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
  Rogers,J. and Bradley,A.
  Direct Submission
  Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
  CB10 1SA, UK. http://www.sanger.ac.uk/MICER
  Location/Qualifiers
    1..769
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /db_xref="taxon:10090"
    /clone="MHPN234h03"
    /clone_1fb="MHPN"

ORIGIN
Query Match      70.0%; Score 21; DB 11; Length 769;
Best Local Similarity 82.8%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      2 ATGCTGTTCACCGTCGTCGTTGTTCCA 30
Db      307 ATCGTGTCCAGCCGTCGTGATGATTCGA 279
|||||
RESULT 14
LOCUS   CC848693/c
DEFINITION
NDL.2114.T7 Notre Dame Liverpool Aedes aegypti genomic clone
Notredame Liverpool-2114, genomic survey sequence.
ACCESSION
CC848693
VERSION  CC848693.1 GI:33197857
KEYWORDS
GSS.
SOURCE   Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
          Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
1 (bases 1 to 832)
  Loftus,B., Shetty,J., Knudson,D. and Severson,D.
  BAC end sequencing of Aedes aegypti
  Unpublished (2003)
  Other_GSSs: NDL.2114.SP6
  Contact: Brendan Loftus
  Department of Eukaryotic Genomics
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-3543
  Fax: 301-838-0208
  Email: entaetigr.org
  Library was provided by David Severson
  Seq primer: T7
  Classes: BAC ends.
  Location/Qualifiers
    1..832
    /organism="Aedes aegypti"
    /mol_type="genomic DNA"
    /db_xref="taxon:10090"
    /clone="NDL.2114"
    /clone_1fb="NDL.2114"
    /clone_2fb="NDL.2114"
    /note="Vector: pECBAC1, Site 1: Hind III; The library was
    prepared from whole body tissue of newly hatched L1 larvae
    by David Severson at the University of Notre Dame and
    Hongbin Zhang"

FEATURES
source
  Location/Qualifiers
    1..832
    /organism="Aedes aegypti"
    /mol_type="genomic DNA"
    /db_xref="taxon:10090"
    /clone="NDL.2114"
    /clone_1fb="NDL.2114"
    /clone_2fb="NDL.2114"
    /note="Vector: pECBAC1, Site 1: Hind III; The library was
    prepared from whole body tissue of newly hatched L1 larvae
    by David Severson at the University of Notre Dame and
    Hongbin Zhang"

FEATURES
source
  Location/Qualifiers
    1..832
    /organism="Aedes aegypti"
    /mol_type="genomic DNA"
    /db_xref="taxon:10090"
    /clone="NDL.2114"
    /clone_1fb="NDL.2114"
    /clone_2fb="NDL.2114"
    /note="Vector: pECBAC1, Site 1: Hind III; The library was
    prepared from whole body tissue of newly hatched L1 larvae
    by David Severson at the University of Notre Dame and
    Hongbin Zhang"

```

```

/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="Notredame Liverpool-2114"
/clone_1fb="Notredame Liverpool"
/clone_2fb="Notredame Liverpool"
/note="Vector: pECBAC1, Site 1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"

ORIGIN
Query Match      70.0%; Score 21; DB 9; Length 832;
Best Local Similarity 82.8%; Pred. No. 2.4e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      2 ATGCTGTTCACCGTCGTCGTTGTTCCA 30
Db      242 ATCGTGTTCACCGTCGTCGTTGATTCGA 214
|||||
RESULT 15
LOCUS   CC860012/c
DEFINITION
NDL.2113.T7 Notre Dame Liverpool Aedes aegypti genomic clone
Notredame Liverpool-2113, genomic survey sequence.
ACCESSION
CC860012
VERSION  CC860012.1 GI:33220222
KEYWORDS
GSS.
SOURCE   Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
          Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
1 (bases 1 to 835)
  Loftus,B., Shetty,J., Knudson,D. and Severson,D.
  BAC end sequencing of Aedes aegypti
  Unpublished (2003)
  Other_GSSs: NDL.2113.SP6
  Contact: Brendan Loftus
  Department of Eukaryotic Genomics
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-3543
  Fax: 301-838-0208
  Email: entaetigr.org
  Library was provided by David Severson
  Seq primer: T7
  Classes: BAC ends.
  Location/Qualifiers
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    /organism="Aedes aegypti"
    /mol_type="genomic DNA"
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    /note="Vector: pECBAC1, Site 1: Hind III; The library was
    prepared from whole body tissue of newly hatched L1 larvae
    by David Severson at the University of Notre Dame and
    Hongbin Zhang"

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    /note="Vector: pECBAC1, Site 1: Hind III; The library was
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    by David Severson at the University of Notre Dame and
    Hongbin Zhang"

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    /clone_2fb="NDL.2114"
    /note="Vector: pECBAC1, Site 1: Hind III; The library was
    prepared from whole body tissue of newly hatched L1 larvae
    by David Severson at the University of Notre Dame and
    Hongbin Zhang"

Search completed: March 6, 2006, 01:57:49
Job time : 141.632 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:54:12 ; Search time 8.38752 Seconds  
(Without alignments)  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Capext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	19.4	64.7	2243	3	US-08-029-170-15
5	19.4	64.7	2243	3	US-09-443-745-15
6	18.8	63.3	4571	3	US-09-949-016-16262
7	18.8	62.7	7812	3	US-09-368-590-1
8	18.8	62.7	8756	3	US-09-949-016-1438
9	18.8	62.7	9541	3	US-08-961-527-132
10	18.8	62.7	112874	3	US-09-949-016-13180
11	18.6	62.0	549	3	US-09-270-767-29480
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13	18.4	61.3	1260	3	US-09-248-7968-3293
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15	18	60.0	601	3	US-09-949-016-200252
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17	18	60.0	889	3	US-08-956-171E-1190
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19	18	60.0	1591	2	US-09-921-992-2
20	18	60.0	33675	3	US-09-949-016-13379
21	18	60.0	111509	3	US-09-832-871-3
22	18	60.0	254366	3	US-09-583-110-1388
23	17.8	59.3	393	3	US-09-107-433-743
24	17.8	59.3	393	3	US-09-107-433-743

25	17.8	59.3	499	3	US-09-270-767-1993	Sequence 1993, App
26	17.8	59.3	499	3	US-09-270-767-17275	Sequence 17275, A
27	17.8	59.3	601	3	US-09-949-016-142937	Sequence 142937, A
28	17.8	59.3	601	3	US-09-949-016-204029	Sequence 204029, A
29	17.8	59.3	601	3	US-09-949-016-204030	Sequence 204030, A
30	17.8	59.3	978	3	US-08-858-207A-174	Sequence 174, App
31	17.8	59.3	999	3	US-08-961-527-193	Sequence 193, App
32	17.8	59.3	2009	2	US-07-958-222A-1	Sequence 1, App11
33	17.8	59.3	8073	3	US-09-949-016-12327	Sequence 12327, A
34	17.8	59.3	8074	3	US-09-949-016-16645	Sequence 16645, A
35	17.8	59.3	9472	2	US-08-325-547-9	Sequence 9, App11
36	17.8	59.3	40505	3	US-09-949-016-13439	Sequence 13439, A
37	17.8	59.3	72843	3	US-09-949-016-12574	Sequence 12574, A
38	17.8	59.3	141115	3	US-09-949-016-13614	Sequence 13614, A
39	17.8	59.3	183202	3	US-09-949-016-13614	Sequence 13614, A
40	17.8	59.3	265038	3	US-09-949-016-15779	Sequence 15779, A
41	17.8	59.3	276237	3	US-09-949-016-17504	Sequence 17504, A
42	17.4	58.0	331	3	US-09-640-211A-169	Sequence 169, App
43	17.4	58.0	601	3	US-09-949-016-178197	Sequence 178197, App
44	17.4	58.0	719	3	US-09-107-433-820	Sequence 820, App
45	17.4	58.0	789	3	US-09-252-991A-11034	Sequence 11034, A

## ALIGNMENTS

RESULT 1  
US-08-880-499-1  
Sequence 1, Application US/08880499  
Patent No. 6037523  
GENERAL INFORMATION:  
APPLICANT: Albertson, Marc C.  
APPLICANT: Fox, Tim W.  
APPLICANT: Carl, Garmaat W.  
APPLICANT: Huffman, Gary A.  
APPLICANT: Kendall, Timmy L.  
TITLE OF INVENTION: MALE TISSUE-PREPARED REGULATORY REGION  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: PIONEER HI-BRED INTERNATIONAL, INC.  
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.  
STREET: Box 1000  
CITY: Johnston  
STATE: Iowa  
COUNTRY: USA  
ZIP: 50131  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,499  
FILING DATE: CONCURRENTLY HERewith  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sweeney, Patricia A.  
REGISTRATION NUMBER: 32,733  
REFERENCE/DOCKET NUMBER: 0578  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (515) 248-4800  
TELEFAX: (515) 248-4844  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1394 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-880-499-1  
Query Match 100.0%; Score 30; DB 3; Length 1394;

Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACCGTTCGCTTGTTC 30  
Db 1179 CATGCTGTTCACCGTTCGCTTGTTC 1208

## RESULT 2

US-08-880-499-2

Sequence 2, Application US/08880499  
Patent No. 6037523

GENERAL INFORMATION:

APPLICANT: Albertson, Marc C.

APPLICANT: Fox, Tim W.

APPLICANT: Carl, Garnat W.

APPLICANT: Huffman, Gary A.

APPLICANT: Kendall, Jimmy L.

TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION

TITLE OF INVENTION: AND METHOD OF USING SAME

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.

STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.

STREET: Box 1000

CITY: Johnston

STATE: Iowa

COUNTRY: USA

ZIP: 50131

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,499

FILING DATE: CONCURRENTLY HERewith

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Sweeney, Patricia A.

REGISTRATION NUMBER: 32,733

REFERENCE/DOCKET NUMBER: 0578

TELECOMMUNICATION INFORMATION:

TELEPHONE: (515) 248-4800

TELEFAX: (515) 248-4844

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1394 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-880-499-2

Query Match 100.0%; Score 30; DB 3; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACCGTTCGCTTGTTC 30  
Db 1179 CATGCTGTTCACCGTTCGCTTGTTC 1208

## RESULT 3

US-07-937-609-15

Sequence 15, Application US/07937609  
Patent No. 5319073

GENERAL INFORMATION:

APPLICANT: MANK, Stephen A.

TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF

TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/937,609

FILING DATE: 19920902

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/831,248

FILING DATE: 07-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/861,769

FILING DATE: 01-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/928,033

FILING DATE: 11-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/166 NIHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300

TELEFAX: (703) 683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 2243 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: rat brain CCKB receptor

FEATURE:

NAME/KEY: CDS

LOCATION: 136..1494

US-07-937-609-15

Query Match 64.7%; Score 19.4; DB 2; Length 2243;

Best Local Similarity 79.3%; Pred. No. 55;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACCGTTCGCTTGTTC 29  
Db 5 CCGCTGTCTCACTCACTCACTGCTTC 33

## RESULT 4

US-08-029-170-15

Sequence 15, Application US/08029170  
Patent No. 6169173

GENERAL INFORMATION:

APPLICANT: MANK, Stephen A.

TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF

TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Foley &amp; Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/029,170  
FILING DATE: 19930310  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,609  
FILING DATE: 02-SEP-1992  
APPLICATION NUMBER: US 07/928,033  
FILING DATE: 11-AUG-1992  
APPLICATION NUMBER: US 07/861,769  
FILING DATE: 01-APR-1992  
APPLICATION NUMBER: US 07/831,248  
FILING DATE: 07-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 40399/166 NIHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2243 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: rat brain CCKB receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 136..1494  
US-08-029-170-15

Query Match 64.7%; Score 19.4; DB 3; Length 2243;  
Best Local Similarity 79.3%; Pred. No. 55;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAGCTGTTCACCGTCTGCTGTC 29  
Db 5 CCGCTGCTCACTCACTGCTGTTTC 33

RESULT 5  
US-09-443-745-15  
Sequence 15, Application US/09443745  
Patent No. 6706493  
GENERAL INFORMATION:  
APPLICANT: MANK, Stephen A.  
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0239  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/443,745

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/029,170  
FILING DATE: 10-MAR-1993  
APPLICATION NUMBER: US 07/937,609  
FILING DATE: 02-SEP-1992  
APPLICATION NUMBER: US 07/928,033  
FILING DATE: 11-AUG-1992  
APPLICATION NUMBER: US 07/861,769  
FILING DATE: 01-APR-1992  
APPLICATION NUMBER: US 07/831,248  
FILING DATE: 07-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 40399/166 NIHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2243 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: rat brain CCKB receptor  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 136..1494  
US-09-443-745-15

Query Match 64.7%; Score 19.4; DB 3; Length 2243;  
Best Local Similarity 79.3%; Pred. No. 55;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAGCTGTTCACCGTCTGCTGTC 29  
Db 5 CCGCTGCTCACTCACTGCTGTTTC 33

RESULT 6  
US-09-949-016-16262  
Sequence 16262, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16262  
LENGTH: 45571  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-16262

Query Match 63.3%; Score 19; DB 3; Length 45571;

Best Local Similarity 81.5%; Pred. No. 1.4e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGCTTGTTCACCGTTGCTTGTTC 29

Db 38119 TGTTGTTCATCGTCTCTCTTCTCC 38145

## RESULT 7

US-09-368-590-1/c  
; Sequence 1, Application US/09368590  
; Patent No. 6187563  
; GENERAL INFORMATION:  
; APPLICANT: Solimena, Michele  
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR  
; FILE REFERENCE: 101918-200 (OCR-941)  
; CURRENT FILING DATE: 1999-08-04  
; EARLIER APPLICATION NUMBER: US/09/368,590  
; EARLIER FILING DATE: 1998-08-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 7812  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(6879)  
; NAME/KEY: unsure  
; LOCATION: (100)...(102)  
; NAME/KEY: unsure  
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; NAME/KEY: unsure  
; LOCATION: (2266)...(2268)  
; US-09-368-590-1

Query Match 62.7%; Score 18.8; DB 3; Length 7812;  
Best Local Similarity 76.7%; Pred. No. 1.3e+02;  
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTGCTTGTTC 30  
Db 841 CATGCTGTTCACGATCGTCTCTCTCA 812

## RESULT 8

US-09-949-016-1438/c  
; Sequence 1438, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1438  
; LENGTH: 8756  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-1438

Query Match 62.7%; Score 18.8; DB 3; Length 8756;

Best Local Similarity 76.7%; Pred. No. 1.3e+02;  
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTGCTTGTTC 30

Db 1912 CATGCTGTTCACGATCGTCTCTCA 1883

## RESULT 9

US-08-961-527-132  
; Sequence 132, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS Version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 132:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9541 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-961-527-132

Query Match 62.7%; Score 18.8; DB 3; Length 9541;  
Best Local Similarity 76.7%; Pred. No. 1.3e+02;  
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTGCTTGTTC 30  
Db 8049 CAGGCTGTTCACGATCGTCTCTCA 8078

## RESULT 10

US-09-949-016-13180/c  
; Sequence 13180, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13180  
LENGTH: 112874  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(112874)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13180

Query Match 62.7%; Score 18.8; DB 3; Length 112874;  
Best Local Similarity 76.7%; Pred. No. 2e+02;  
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CAGCTTGTCAACCGTTCGTTGTTCCA 30  
Db 41167 CAGCTTGTCAACCGTTCGTTGTTCCA 41138

RESULT 11  
US-09-270-767-29480/c  
Sequence 29480, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29480  
LENGTH: 549  
TYPE: DNA  
ORGANISM: *Drosophila melanogaster*  
US-09-270-767-29480

Query Match 62.0%; Score 18.6; DB 3; Length 549;  
Best Local Similarity 84.0%; Pred. No. 98;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCTTGTCAACCGTTCGTTGTT 27  
Db 223 TGCTTGTCAACCGTTCGTTGTT 199

RESULT 12  
US-09-270-767-13492/c  
Sequence 13492, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13492  
LENGTH: 1120  
TYPE: DNA  
ORGANISM: *Drosophila melanogaster*  
US-09-270-767-13492

Query Match 62.0%; Score 18.6; DB 3; Length 1120;  
Best Local Similarity 84.0%; Pred. No. 1.1e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCTTGTCAACCGTTCGTTGTT 27  
Db 223 TGCTTGTCAACCGTTCGTTGTT 199

RESULT 13  
US-09-248-796A-3293  
Sequence 3293, Application US/09248796A  
Patent No. 6747132  
GENERAL INFORMATION:  
APPLICANT: Keith Weinstein et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 3293  
LENGTH: 1260  
TYPE: DNA  
ORGANISM: *Candida albicans*  
US-09-248-796A-3293

Query Match 61.3%; Score 18.4; DB 3; Length 1260;  
Best Local Similarity 78.6%; Pred. No. 1.4e+02;  
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCTTGTCAACCGTTCGTTGTTCCA 30  
Db 903 TGCTTGTCAACCGTTCGTTGTTCCA 930

RESULT 14  
US-09-573-080A-7/c  
Sequence 7, Application US/09573080A  
Patent No. 6828097  
GENERAL INFORMATION:  
APPLICANT: JOAN, KNOEL  
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING  
FILE REFERENCE: 30307  
CURRENT APPLICATION NUMBER: US/09/573,080A  
CURRENT FILING DATE: 2000-05-16  
NUMBER OF SEQ ID NOS: 479  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 2710  
TYPE: DNA  
ORGANISM: *Homo sapiens*  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: (1)..(2710)  
OTHER INFORMATION: charlie3  
NAME/KEY: misc feature  
OTHER INFORMATION: n is a, c, g or t  
PUBLICATION INFORMATION:  
AUTHORS: Jurka, J; Malchukiewicz, J; Milosavljevic, A  
TITLE: Prototypic sequences for human repetitive DNA  
JOURNAL: Journal of Molecular Evolution  
VOLUME: 35  
ISSUE: 4  
PAGES: 286-291  
DATE: 1992-10-  
DATABASE ACCESSION NUMBER: Database for repetitive elements (repbase)  
DATABASE ENTRY DATE: 1996-01-26  
US-09-573-080A-7



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 23:29:31 ; Search time 43.1372 Seconds  
(without alignments)  
5750.985 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1179\_1208

Perfect score: 1 catcgttgcacacgttcgttcgttcca 30

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications\_NA\_Main:  
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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	30	100.0	8 US-10-713-381-4	Sequence 4, Appli
2	30	100.0	255 8 US-10-713-381-9	Sequence 9, Appli
3	30	100.0	1394 8 US-10-713-381-1	Sequence 1, Appli
4	30	100.0	1394 8 US-10-713-381-2	Sequence 2, Appli
5	24.2	80.7	158 8 US-10-713-381-3	Sequence 3, Appli
6	22	73.3	1304 5 US-10-001-857-90	Sequence 90, Appli
7	21	70.0	1980090 8 US-10-719-993-6815	Sequence 6815, Ap
8	21	70.0	1542 3 US-10-741-600-17676	Sequence 17676, A
9	20.4	68.0	1542 3 US-09-938-8428-1624	Sequence 1624, Ap
10	20.4	68.0	1542 3 US-09-938-8428-1624	Sequence 1624, Ap
11	20.2	67.3	2397 7 US-10-282-1228-11883	Sequence 11883, A
12	20	66.7	2000 7 US-10-280-318-1785	Sequence 1785, Ap
13	19.6	65.3	940 7 US-10-437-963-96639	Sequence 96639, A
14	19.6	65.3	940 7 US-10-437-963-96639	Sequence 96639, A
15	19.6	65.3	2000 7 US-10-425-115-3534	Sequence 3534, Ap
16	19.4	64.7	2243 3 US-10-260-238-1977	Sequence 1977, Ap
17	19.4	64.7	2243 3 US-10-260-238-1977	Sequence 15, Appli
18	19.4	64.7	2256646 7 US-11-063-391-5	Sequence 1, Appli
19	19	63.3	622 4 US-10-470-565-1	Sequence 5, Appli
20	19	63.3	964 4 US-09-925-065A-863989	Sequence 863989, A
21	19	63.3	1041 8 US-09-925-065A-546217	Sequence 546217, A
22	19	63.3	1821 7 US-10-425-115-100318	Sequence 100318, A
23	19	63.3	1821 9 US-10-425-563-5	Sequence 5, Appli

c 24	19	63.3	5671	3	US-09-764-872-729	Sequence 729, App
c 25	19	63.3	198522	5	US-10-087-192-244	Sequence 244, App
c 26	18.8	62.7	520	4	US-09-925-065A-472473	Sequence 472473, A
c 27	18.8	62.7	593	4	US-09-925-065A-936359	Sequence 936359, A
c 28	18.8	62.7	593	4	US-09-925-065A-936360	Sequence 936360, A
c 29	18.8	62.7	593	4	US-09-925-065A-936397	Sequence 936397, A
c 30	18.8	62.7	883	3	US-09-938-453-279	Sequence 279, App
c 31	18.8	62.7	883	3	US-10-225-068-183	Sequence 183, App
c 32	18.8	62.7	883	6	US-10-225-068-183	Sequence 911, App
c 33	18.8	62.7	883	7	US-10-374-780A-381	Sequence 381, App
c 34	18.8	62.7	883	9	US-10-225-068-183	Sequence 971, App
c 35	18.8	62.7	883	9	US-10-225-068-183	Sequence 781, App
c 36	18.8	62.7	1083	3	US-09-815-242-7281	Sequence 22639, A
c 37	18.8	62.7	1083	7	US-10-282-1228-22639	Sequence 2194, App
c 38	18.8	62.7	1083	7	US-10-335-977-2194	Sequence 2195, App
c 39	18.8	62.7	1125	7	US-10-437-963-40048	Sequence 40048, A
c 40	18.8	62.7	1856	7	US-10-472-928-2217	Sequence 2217, App
c 41	18.8	62.7	1899	8	US-10-472-928-2217	Sequence 9220, App
c 42	18.8	62.7	1902	3	US-09-815-242-9220	Sequence 37788, A
c 43	18.8	62.7	2000	7	US-10-282-1228-37788	Sequence 2535, App
c 44	18.8	62.7	2000	7	US-10-280-238-2535	Sequence 33483, A
c 45	18.8	62.7	2247	6	US-10-369-493-33483	

## ALIGNMENTS

RESULT 1  
US-10-713-381-4  
Sequence 4, Application US/10713381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
TITLE OF INVENTION: USING SAME  
FILE REFERENCE: 5768  
CURRENT APPLICATION NUMBER: US/10/713.381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880.499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-4

Query Match 100.0% Score 30; DB 8; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.008;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CATCCTTGTTCACCGTTCGTTGTTCCA 30  
1 CATCCTTGTTCACCGTTCGTTGTTCCA 30

RESULT 2  
US-10-713-381-9  
Sequence 9, Application US/10713381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
TITLE OF INVENTION: USING SAME

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; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-713-381-9

Query Match
Best Local Similarity 100.0%; Score 30; DB 8; Length 255;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTCGTTGTTCCA 30
Db 39 CATGCTGTTCACCGTTCGTTGTTCCA 68

RESULT 3
US-10-713-381-1
; Sequence 1, Application US/10/713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-713-381-1

Query Match
Best Local Similarity 100.0%; Score 30; DB 8; Length 1394;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTCGTTGTTCCA 30
Db 1179 CATGCTGTTCACCGTTCGTTGTTCCA 1208

RESULT 4
US-10-713-381-2
; Sequence 2, Application US/10/713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-713-381-2

Query Match
Best Local Similarity 100.0%; Score 30; DB 8; Length 1394;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTCGTTGTTCCA 30
Db 1179 CATGCTGTTCACCGTTCGTTGTTCCA 1208

RESULT 5
US-10-713-381-3
; Sequence 3, Application US/10/713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-713-381-3

Query Match
Best Local Similarity 89.7%; Score 24.2; DB 8; Length 158;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTCGTTGTTCC 29
Db 25 CATGCTGTTCACCGTTCGTTGTTCC 53

RESULT 6
US-10-001-857-90/C
; Sequence 90, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Proce
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001.857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 1304
; TYPE: DNA
; ORGANISM: Homo sapien
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US-10-001-857-90

Query Match 73.3%; Score 22; DB 5; Length 1304;  
Best Local Similarity 83.3%; Pred. No. 11;  
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTCGCTGTTCACCA 30  
DB 1155 CTTCTGTTCCTCCCGCTTCCTGTTCACCA 1126

RESULT 7

US-10-719-993-6815/C  
Sequence 6815, Application US/10719993  
Publication No. US20040265849A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CL001496  
CURRENT APPLICATION NUMBER: US/10/719,993  
CURRENT FILING DATE: 2003-11-24  
NUMBER OF SEQ ID NOS: 55342  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6815  
LENGTH: 1980090  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1980090)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-719-993-6815

Query Match 70.0%; Score 21; DB 8; Length 1980090;  
Best Local Similarity 82.8%; Pred. No. 2,2e+02;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGCTGTTCACCA 30  
DB 1948918 ATTCTGTTCACGATTCGCTGTTCACCA 1948890

RESULT 8

US-10-741-600-17676/C  
Sequence 17676, Application US/10741600  
Publication No. US20050026169A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: CL001499  
CURRENT APPLICATION NUMBER: US/10/741,600  
CURRENT FILING DATE: 2003-12-22  
NUMBER OF SEQ ID NOS: 73997  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17676  
LENGTH: 1980090  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1980090)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-741-600-17676

Query Match 70.0%; Score 21; DB 8; Length 1980090;  
Best Local Similarity 82.8%; Pred. No. 2,2e+02;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGCTGTTCACCA 30  
DB 1948918 ATTCTGTTCACGATTCGCTGTTCACCA 1948890

RESULT 9...  
US-09-938-842A-1624  
Sequence 1624, Application US/09938842A  
Patent No. US20020160378A1  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
FILE REFERENCE: SCRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 1624  
LENGTH: 1542  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1624

Query Match 68.0%; Score 20.4; DB 3; Length 1542;  
Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTCGCTGTTCACCA 30  
DB 237 CATGATGTTCACCAATCGTGTTCACCA 266

RESULT 10

US-09-938-842A-1624  
Sequence 1624, Application US/09938842A  
Publication No. US2004009476A9  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
FILE REFERENCE: SCRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 1624  
LENGTH: 1542  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1624

Query Match 68.0%; Score 20.4; DB 3; Length 1542;  
Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CATGCTGTTCACCGTTCGCTGTTCACCA 30  
DB 237 CATGATGTTCACCAATCGTGTTCACCA 266

RESULT 11  
US-10-282-122A-31883  
Sequence 31883, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyklich, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: EITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 31883  
LENGTH: 2397  
TYPE: DNA  
ORGANISM: Pseudomonas putida  
US-10-282-122A-31883

Query Match 67.3%; Score 20.2; DB 7; Length 2397;  
Best Local Similarity 88.0%; Pred. No. 2e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATGCTGTTCAACCGTTCGCTTG 25  
DB 516 CATGCTGTTCAACCGTTCGCTTG 540

RESULT 12  
US-10-260-238-1785  
Sequence 1785, Application US/10260238  
Publication No. US20040016025A1  
GENERAL INFORMATION:  
APPLICANT: Budworth, Paul R.  
APPLICANT: Moughamer, Todd G.  
APPLICANT: Briggs, Steven P.  
APPLICANT: Cooper, Bret  
APPLICANT: Glazebrook, Jane  
APPLICANT: Goff, Stephen A.  
APPLICANT: Katagiri, Fumiyaki  
APPLICANT: Krepe, Joel

APPLICANT: Provart, Nicholas  
APPLICANT: Ricke, Darrell  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
FILE REFERENCE: 6011-NP  
CURRENT APPLICATION NUMBER: US/10/260,238  
CURRENT FILING DATE: 2002-09-26  
PRIOR APPLICATION NUMBER: US 60/325,448  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/325,277  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/370,620  
PRIOR FILING DATE: 2002-04-04  
NUMBER OF SEQ ID NOS: 6077  
SEQ ID NO 1785  
LENGTH: 2000  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-10-260-238-1785

Query Match 66.7%; Score 20; DB 7; Length 2000;  
Best Local Similarity 82.1%; Pred. No. 2.3e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGCTTGTTCAACCGTTCGCTTGTTCGA 30  
DB 1179 TACATGTTTAAACCGTTCGCTTATTCGA 1206

RESULT 13  
US-10-437-963-96639/c  
Sequence 96639, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 96639  
LENGTH: 640  
TYPE: DNA  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_94716C.1  
US-10-437-963-96639

Query Match 65.3%; Score 19.6; DB 7; Length 640;  
Best Local Similarity 84.6%; Pred. No. 2.9e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CTGTTCAACCGTTCGCTTGTTCGA 30  
DB 199 CATGTTTAAACCGTTCGCTTATTCGA 174

RESULT 14  
US-10-425-115-3534/c  
Sequence 3534, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 3534  
LENGTH: 901  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_103225C.1  
US-10-425-115-3534

Query Match  
Best Local Similarity 65.3%; Score 19.6; DB 8; Length 901;  
Best Local Similarity 84.6%; Pred. No. 3.1e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACCGTTCCTTGT 26  
Db 33 CACGCTTGTTCACCGTTCCTTGT 8

RESULT 15  
US-10-260-238-1977/c  
Sequence 1977, Application US/10260238  
Publication No. US20040016025A1  
GENERAL INFORMATION:  
APPLICANT: Budworth, Paul R.  
APPLICANT: Moushamer, Todd G.  
APPLICANT: Briggs, Steven P.  
APPLICANT: Cooper, Bret  
APPLICANT: Glazedrook, Jane  
APPLICANT: Golt, Stephen A.  
APPLICANT: Katagiri, Rumiyaeki  
APPLICANT: Kreps, Joel  
APPLICANT: Provart, Nicholas  
APPLICANT: Rike, Darrell  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
FILE REFERENCE: 6011-NP  
CURRENT APPLICATION NUMBER: US/10/260,238  
CURRENT FILING DATE: 2002-09-26  
PRIOR APPLICATION NUMBER: US 60/325,448  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/325,277  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/370,620  
PRIOR FILING DATE: 2002-04-04  
NUMBER OF SEQ ID NOS: 6077  
SEQ ID NO 1977  
LENGTH: 2000  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-10-260-238-1977

Query Match  
Best Local Similarity 65.3%; Score 19.6; DB 7; Length 2000;  
Best Local Similarity 84.6%; Pred. No. 3.4e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CTGTTCACCGTTCGTTGTTCCA 30  
Db 291 CATGTTACCGTTCGTTATTCA 266

Search completed: March 6, 2006, 03:55:17  
Job time: 45.1372 secs

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OM nucleic - nucleic search, using sw model

Run on: March 6, 2006, 01:58:03 ; Search time 31.166 Seconds  
(without alignments)  
2100.307 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1179\_1208

Sequence: 1 catgctgttcacacgcgtcgtcgttcac 30

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/FC1\_NEW\_PUB.seq.\*  
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6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
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10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
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12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
2	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
3	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
4	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
5	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
6	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
7	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
8	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
9	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
10	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
11	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
12	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
13	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
14	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
15	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
16	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
17	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
18	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
19	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap
20	19.4	64.7	2422	12 US-11-136-527-2272	Sequence 863989, Ap

21	18	60.0	572	6 US-09-925-065A-819344	Sequence 819344, A
22	18	60.0	573	6 US-09-925-065A-821053	Sequence 821053, A
23	18	60.0	1395	6 US-09-925-065A-30378	Sequence 30378, A
24	18	60.0	1395	6 US-09-925-065A-30379	Sequence 30379, A
25	17.8	59.3	201	8 US-10-995-561-9774	Sequence 9774, A
26	17.8	59.3	201	8 US-10-995-561-9774	Sequence 9774, A
27	17.8	59.3	201	8 US-10-995-561-9787	Sequence 9787, A
28	17.8	59.3	201	8 US-10-995-561-52210	Sequence 52210, A
29	17.8	59.3	603	6 US-09-925-065A-826915	Sequence 826915, A
30	17.8	59.3	617	6 US-09-925-065A-673672	Sequence 673672, A
31	17.8	59.3	617	6 US-09-925-065A-673672	Sequence 673672, A
32	17.8	59.3	1385	6 US-09-925-065A-667982	Sequence 667982, A
33	17.8	59.3	1907	12 US-11-010-239-68	Sequence 68, App1
34	17.8	59.3	2039	6 US-09-925-065A-704153	Sequence 704153, A
35	17.8	59.3	2039	6 US-09-925-065A-704154	Sequence 704154, A
36	17.8	59.3	2039	6 US-09-925-065A-704155	Sequence 704155, A
37	17.8	59.3	2867	8 US-10-995-561-357	Sequence 357, App
38	17.8	59.3	3431	8 US-10-995-561-358	Sequence 358, App
39	17.8	59.3	9474	12 US-11-155-232-1	Sequence 1, App1
40	17.8	59.3	45038	8 US-10-995-561-13311	Sequence 13311, A
41	17.8	59.3	81210	8 US-10-995-561-13295	Sequence 13295, A
42	17.8	59.3	163317	12 US-11-117-167-212	Sequence 212, App
43	17.8	59.3	171732	12 US-11-121-086-98	Sequence 98, App1
44	17.8	59.3	1082144	12 US-11-117-187-211	Sequence 211, App
45	17.6	58.7	600	12 US-11-136-527-7828	Sequence 7828, App

## ALIGNMENTS

RESULT 1  
US-11-136-527-2272  
Sequence 2272, Application US/1136527  
Publication No. US2005028570A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
FILE REFERENCE: 031896-041000 (AM101086)  
CURRENT APPLICATION NUMBER: US/11/136,527  
PRIOR FILING DATE: 2005-05-25  
PRIOR APPLICATION NUMBER: US 60/574,294  
PRIOR FILING DATE: 2005-05-26  
NUMBER OF SEQ ID NOS: 362830  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2272  
LENGTH: 2422  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-11-136-527-2272  
Query Match 64.7%; Score 19.4; DB 12; Length 2422;  
Best Local Similarity 79.3%; Pred. No. 28;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Db 1 CAGGCTTTCACACGCTTCGCTTC 29  
5 CCGGCTTCACACGCTTCGCTTC 33  
RESULT 2  
US-09-925-065A-863989  
Sequence 863989, Application US/09925065A,  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24

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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 863989
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-863989
```

```

Query Match      63.3%; Score 19; DB 6; Length 622;
Best Local Similarity 81.5%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

Qy      2 ATGCTGTTCACCGTTCGTTGTTTC 28
Db      400 AGCTAGTCCACCTTTGTCTTGTTC 426
```

```

RESULT 3
US-09-925-065A-546217
; Sequence 546217, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 546217
;   LENGTH: 964
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-546217
```

```

Query Match      63.3%; Score 19; DB 6; Length 964;
Best Local Similarity 81.5%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

Qy      2 ATGCTGTTCACCGTTCGTTGTTTC 28
Db      256 AGCTAGTCCACCTTTGTCTTGTTC 282
```

```

RESULT 4
US-11-197-133A-5/C
; Sequence 5, Application US/11197133A
; Publication No. US20060040361A1
; GENERAL INFORMATION:
;   APPLICANT: De Le Fuente Jose de Jesus
;   APPLICANT: Kocan Katherine M.
;   APPLICANT: Garcia-Almazan Consuelo
;   APPLICANT: Blouin Edwin F.
;   TITLE OF INVENTION: Protective antigens and vaccines for the control of multi species
```

```

; TITLE OF INVENTION: Infestations
; FILE REFERENCE: 57338/05-261
; CURRENT APPLICATION NUMBER: US/11/197,133A
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US 10/972769
; PRIOR FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: US 10/425563
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/376251
; PRIOR FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Ixodes scapularis
```

```

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1487)..(1487)
OTHER INFORMATION: n is a c g o r t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1595)..(1595)
OTHER INFORMATION: n is a c g o r t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1606)..(1606)
OTHER INFORMATION: n is a c g o r t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1623)..(1623)
OTHER INFORMATION: n is a c g o r t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1762)..(1762)
OTHER INFORMATION: n is a c g o r t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1789)..(1789)
OTHER INFORMATION: n is a c g o r t
US-11-197-133A-5
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```

Query Match      63.3%; Score 19; DB 9; Length 1821;
Best Local Similarity 81.5%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

Qy      3 TGCTGTTCACCGTTCGTTGTTTC 29
Db      914 TGCTGTTCACCGTTCGTTGTTTC 888
```

```

RESULT 5
US-09-925-065A-472473/C
; Sequence 472473, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   FILE REFERENCE: 108827.135
;   CURRENT APPLICATION NUMBER: US/09/925,065A
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 60/243,096
;   PRIOR FILING DATE: 2000-10-24
;   PRIOR APPLICATION NUMBER: US 60/252,147
;   PRIOR FILING DATE: 2000-11-20
;   PRIOR APPLICATION NUMBER: US 60/250,092
;   PRIOR FILING DATE: 2000-11-30
;   PRIOR APPLICATION NUMBER: US 60/261,766
;   PRIOR FILING DATE: 2001-01-16
;   PRIOR APPLICATION NUMBER: US 60/289,846
;   PRIOR FILING DATE: 2001-05-09
;   NUMBER OF SEQ ID NOS: 957086
```

```
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 472473
LENGTH: 520
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-472473
```

```
Query Match          62.7%; Score 18.8; DB 6; Length 520;
Best Local Similarity 76.7%; Pred. No. 37;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 CATGCTTGTTCACCGTTCCTGTTGTTCCA 30
DB      211 CATGCTTGTTCACCGTTCCTGTTGTTCCA 182
```

```
RESULT 6
US-09-925-065A-936359
Sequence 936359, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
```

```
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 936359
LENGTH: 593
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-936359
```

```
Query Match          62.7%; Score 18.8; DB 6; Length 593;
Best Local Similarity 76.7%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 CATGCTTGTTCACCGTTCCTGTTGTTCCA 30
DB      341 CATCTCTCACCCTCTGCTTTGTGTTCCA 370
```

```
RESULT 7
US-09-925-065A-936360
Sequence 936360, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
```

```
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
```

```
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 936360
LENGTH: 593
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-936360
```

```
Query Match          62.7%; Score 18.8; DB 6; Length 593;
Best Local Similarity 76.7%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 CATGCTTGTTCACCGTTCCTGTTGTTCCA 30
DB      341 CATCTCTCACCCTCTGCTTTGTGTTCCA 370
```

```
RESULT 8
US-09-925-065A-953397
Sequence 953397, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
```

```
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 953397
LENGTH: 593
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-953397
```

```
Query Match          62.7%; Score 18.8; DB 6; Length 593;
Best Local Similarity 76.7%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 CATGCTTGTTCACCGTTCCTGTTGTTCCA 30
DB      341 CATCTTGTTCACCGCTCTGCTTTGTGTTCCA 370
```

```
RESULT 9
US-10-523-503-37/C
Sequence 37, Application US/10523503
Publication No. US20060037102A1
GENERAL INFORMATION:
```

```
APPLICANT: BASF PLANT SCIENCE GMBH
TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS IV
FILE REFERENCE: 16313-0236
CURRENT FILING DATE: 2005-02-02
PRIOR APPLICATION NUMBER: US 10/523,503
PRIOR FILING DATE: 2002-06-02
PRIOR APPLICATION NUMBER: US 60/400,803
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn version 3.2
SEQ ID NO 37
LENGTH: 1908
```

TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-10-523-503-37

Query Match 62.7%; Score 18.8; DB 7; Length 1908;  
Best Local Similarity 76.7%; Pred. No. 51;  
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATGCTTTCACCGTTCGCTTGTTC 30  
Db 1688 CTTCCTTCCTTCGACCGTTCCTTTGTTC 1659

RESULT 10  
US-10-330-773-86/c  
Sequence 86, Application US/10330773  
Publication No. US20060040262A1  
GENERAL INFORMATION:  
APPLICANT: David W. Morris  
APPLICANT: Marc Malandro  
TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
FILE REFERENCE: 529452001300  
CURRENT APPLICATION NUMBER: US/10/330,773  
CURRENT FILING DATE: 2002-12-27  
NUMBER OF SEQ ID NOS: 981  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 86  
LENGTH: 128963  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(128963)  
OTHER INFORMATION: n = A,T,C or G  
US-10-330-773-86

Query Match 62.7%; Score 18.8; DB 7; Length 128963;  
Best Local Similarity 76.7%; Pred. No. 1.5e+02;  
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATGCTTTCACCGTTCGCTTGTTC 30  
Db 102327 CAACTTCTTCACCGTTCATGTTCACA 102298

RESULT 11  
US-09-925-065A-811550  
Sequence 811550, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 811550  
LENGTH: 599  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-811550

Query Match 61.3%; Score 18.4; DB 6; Length 599;  
Best Local Similarity 78.6%; Pred. No. 59;  
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCCTGTTCAACCGTTCGCTTGTTC 30  
Db 504 TGCTGCTCAACCGTTCGCTTGTTC 531

RESULT 12  
US-09-925-065A-772237  
Sequence 772237, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 772237  
LENGTH: 624  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-772237

Query Match 61.3%; Score 18.4; DB 6; Length 624;  
Best Local Similarity 78.6%; Pred. No. 60;  
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCTGTTCAACCGTTCGCTTGTTC 29  
Db 49 ATTTGTTCAACCGTTCGCTTGTTC 76

RESULT 13  
US-09-925-065A-787145/c  
Sequence 787145, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 787145  
LENGTH: 629

TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-787145

Query Match 61.3%; Score 18.4; DB 6; Length 629;  
Best Local Similarity 78.6%; Pred. No. 60;  
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCTGTTCAACCGTTCGTCCTGTTCC 29  
DB 576 ATTCTGTTCAACGTTTCGTCCTGTTTC 549

## RESULT 14

US-09-925-065A-423  
Sequence 423, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 423  
LENGTH: 642  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-423

Query Match 61.3%; Score 18.4; DB 6; Length 642;  
Best Local Similarity 78.6%; Pred. No. 60;  
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TGCTGTTCAACCGTTCGTCCTGTTCC 30  
DB 295 TGCTGTTCAACGTTTCGTCCTGTTCC 322

RESULT 15  
US-10-750-185-52713  
Sequence 52713, Application US/10750185  
Publication No. US20050260603A1  
GENERAL INFORMATION:  
APPLICANT: MMT GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 52713  
LENGTH: 1012

TYPE: DNA  
ORGANISM: Bovine 1986881292329  
US-10-750-185-52713

Query Match 61.3%; Score 18.4; DB 8; Length 1012;  
Best Local Similarity 78.6%; Pred. No. 67;  
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCTGTTCAACCGTTCGTCCTGTTCC 29  
DB 454 ATTCTGTTCAACGTTTCGTCCTGTTCC 481

Search completed: March 6, 2006, 10:32:51  
Job time : 31.3166 secs

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ORGANISM Zea mays  
REFERENCE 1  
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)  
FEATURES location/Qualifiers  
source 1..50  
/organism="Zea mays"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:4577"

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Query Match 100.0%; Score 40; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40  
11 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 50

Db

RESULT 3  
LOCUS AX224396 158 bp DNA linear PAT 10-SEP-2001  
DEFINITION Sequence 3 from Patent WO0160997.  
ACCESSION AX224396  
VERSION AX224396.1 GI:15554638  
KEYWORDS  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE 1  
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)  
FEATURES location/Qualifiers  
source 1..158  
/organism="Zea mays"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:4577"

ORIGIN  
Query Match 100.0%; Score 40; DB 6; Length 158;  
Best Local Similarity 100.0%; Pred. No. 8.6e-05;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40  
86 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 125

Db

RESULT 4  
LOCUS AX224402 255 bp DNA linear PAT 10-SEP-2001  
DEFINITION Sequence 9 from Patent WO0160997.  
ACCESSION AX224402  
VERSION AX224402.1 GI:15554644  
KEYWORDS  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE 1  
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.  
TITLE Male tissue-preferred regulatory region and method of using same

JOURNAL Patent: WO 0160997-A 9 23-AUG-2001;  
PIONEER HI-BRED INTERNATIONAL, INC. (US)  
FEATURES location/Qualifiers  
source 1..255  
/organism="Zea mays"  
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/db\_xref="taxon:4577"

ORIGIN  
Query Match 100.0%; Score 40; DB 6; Length 255;  
Best Local Similarity 100.0%; Pred. No. 8e-05;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40  
99 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 138

Db

RESULT 5  
LOCUS BD062176 1394 bp DNA linear PAT 27-AUG-2002  
DEFINITION Male tissue-preferred regulatory region and method of using same.  
ACCESSION BD062176  
VERSION BD062176.1 GI:22607781  
KEYWORDS JP 2001520523-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and Kendall,T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL PIONEER HI-BRED INTERNATIONAL INC  
COMMENT PN JP 2001520523-A/1  
PD 30-OCT-2001  
PF 19-JUN-1998 JP 1999504910  
PR 23-JUN-1997 US 08/880499  
PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAAT,GARY A HUFFMAN,  
PI TIMMY L KENDALL  
PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC  
PC C07K14/34,C12Q1/68,  
PC A01H5/00  
CC Strandedness: Single;  
CC Topology: Linear;  
FH key location/Qualifiers  
FEATURES location/Qualifiers  
source 1..1394  
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/db\_xref="taxon:9606"

ORIGIN  
Query Match 100.0%; Score 40; DB 6; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40  
1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

Db

RESULT 6  
LOCUS BD062177 1394 bp DNA linear PAT 27-AUG-2002  
DEFINITION Male tissue-preferred regulatory region and method of using same.  
ACCESSION BD062177  
VERSION BD062177.1 GI:22607782  
KEYWORDS JP 2001520523-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
JOURNAL  
COMMENT  
TITLE  
Male tissue-preferred regulatory region and method of using same  
PIONEER HI-BRED INTERNATIONAL INC  
JP 2001520523-A/2  
PD 30-OCT-2001  
PF 19-JUN-1998 JP 199504910  
PR 23-JUN-1997 US 08/880499  
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAT, GARY A HUFFMAN,  
PI TIMMY L KENDALL  
PC C12N15/82, C12N15/29, C12N9/24, C12N9/10, C12N9/00 PC  
PC C07K14/34, C12Q1/68,  
PC A01H5/00  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES  
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Query Match  
Best Local Similarity 100.0%; Score 40; DB 6; Length 1394;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 AGGATACCTACTCCCAACATCCATCTTACTGATGCAAC 40  
1239 AGGATACCTACTCCCAACATCCATCTTACTGATGCAAC 1278  
RESULT 7  
LOCUS AX224394 1394 bp DNA linear PAT 10-SEP-2001  
DEFINITION Sequence 1 from Patent WO0160997.  
ACCESSION AX224394  
VERSION AX224394.1 GI:15554636  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
AUTHORS  
JOURNAL  
TITLE  
Male tissue-preferred regulatory region and method of using same  
Patent: WO 0160997-A 1 23-AUG-2001;  
PIONEER HI-BRED INTERNATIONAL, INC. (US)  
FEATURES  
source  
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Query Match  
Best Local Similarity 100.0%; Score 40; DB 6; Length 1394;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY  
1 AGGATACCTACTCCCAACATCCATCTTACTGATGCAAC 40  
1239 AGGATACCTACTCCCAACATCCATCTTACTGATGCAAC 1278  
RESULT 8  
LOCUS AX224395 1394 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 2 from Patent WO0160997.  
ACCESSION AX224395  
VERSION AX224395.1 GI:15554637  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
AUTHORS  
JOURNAL  
TITLE  
Male tissue-preferred regulatory region and method of using same  
Patent: WO 0160997-A 2 23-AUG-2001;  
PIONEER HI-BRED INTERNATIONAL, INC. (US)  
FEATURES  
source  
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ORIGIN  
Query Match  
Best Local Similarity 100.0%; Score 40; DB 6; Length 1394;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY  
1 AGGATACCTACTCCCAACATCCATCTTACTGATGCAAC 40  
1239 AGGATACCTACTCCCAACATCCATCTTACTGATGCAAC 1278  
RESULT 9  
LOCUS AF360356 3343 bp DNA linear PLN 12-MAY-2001  
DEFINITION Zea mays male fertility protein (M645) gene, complete cds.  
ACCESSION AF360356  
VERSION AF360356.1 GI:14028756  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
AUTHORS  
JOURNAL  
TITLE  
Unpublished  
Fox, T.W., Trimmell, M.R. and Albertsen, M.C.  
2 (bases 1 to 3343)  
Fox, T.W., Trimmell, M.R. and Albertsen, M.C.  
Direct Submission  
Submitted (13-MAR-2001) Trait and Technology Development, Pioneer  
Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,  
IA 50131-1004, USA  
FEATURES  
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DYPVGHLEAPVGVGWSWPRDNASRLRGRGFEVGVFPEISIFPDLOGRGPVAGIA  
DGVVVRMGEBAGMETFAVNPMDWSERVCAVNSVTRKHEKEPECGRPLGRFGE







RESULT 12  
AC156670  
LOCUS  
DEFINITION  
AC156670.2 GI:58266432  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

303308 bp DNA linear HNG 01-JUL-2005  
\*\*\* SEQUENCING IN PROGRESS \*\*\* 48

AC156670  
unordered pieces.  
Bos taurus clone CH240-60K24

HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
Bos taurus (cow)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE  
AUTHORS

Muzny, D., Maric, M., Metzger, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsdorfs, S., Amin, A., Anguiano, D., Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biewald, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, V., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Day-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G., Fernandez, S., Finley, M., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Gant, R., Garcia, A., Garner, T., Garza, M., Gargiolo, G., Geier, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunatratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hodges, M., Hollins, B., Howells, S., Hulys, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpethy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Koyas, C., Kowik, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, X., London, P., Longacre, S., Lopez, J., Lorenshew, L., Louis, G., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Matlone, E., McWhiney, S., McLeod, M. P., McNeill, T. Z., Meenan, J., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Noster, K., Noster, K., Noster, K., Okunolu, G., Olarnunagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L., Plazo, M., Quiroz, J., Rachlin, E., Reeves, K., Reiger, M. A., Reigh, R., Rieley, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, E., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, M., Saverly, G., Scheer, S., Scott, G., Shattman, S., Shen, H., Shetty, J., Shvartsberg, A., Sisson, I., Sitter, C. D., Smals, D., Sneed, A., Sodergren, E., Song, X. Z., Sorelle, R., Soth, A. J., Steinhilber, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 303308)  
Direct Submission  
Submitted (03-FEB-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

3 (bases 1 to 303308)  
Cow Genome Sequencing Consortium.  
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jun 28, 2005 this sequence version replaced gi:58531390.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
Project Information  
Center project name: FDUJ  
Center clone name: CH240-60K24  
----- Summary Statistics  
Assembly program: Atlas 3.0  
Consensus quality: 284059 bases at least Q40  
Consensus quality: 288397 bases at least Q30  
Consensus quality: 292413 bases at least Q20  
Estimated insert size: 289468; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length  
\* See [http://www.hgsc.bcm.tmc.edu/docs/Gendrak\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Gendrak_draft_data.html))  
NOTE: This sequence may represent more than one clone.  
NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1	4448	contig of 4448 bp in length
*	4449	4498: gap of 50 bp
*	4499	14243: contig of 9745 bp in length
*	14244	14293: gap of 50 bp
*	14294	35389: contig of 21076 bp in length
*	35370	35419: gap of 50 bp
*	35420	47505: contig of 12086 bp in length
*	47506	47555: gap of 50 bp
*	47556	49432: contig of 1877 bp in length
*	49433	49482: gap of 50 bp
*	49483	51615: contig of 2133 bp in length
*	51616	52521: gap of 906 bp
*	52522	59438: contig of 6917 bp in length
*	59439	59488: gap of 50 bp
*	59489	64821: contig of 5333 bp in length
*	64822	64871: gap of 50 bp
*	64872	74540: contig of 9669 bp in length
*	74541	74590: gap of 50 bp
*	74591	90360: contig of 15770 bp in length
*	90361	90833: gap of 473 bp
*	90834	100046: contig of 9213 bp in length
*	100047	100096: gap of 50 bp
*	100097	104650: contig of 4554 bp in length
*	104651	104950: gap of 300 bp
*	104951	106450: contig of 1500 bp in length
*	106451	106608: gap of 158 bp
*	106609	109787: contig of 3179 bp in length



gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

#### ANNOTATION OF FEATURES:

STSs are identified using EPCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: [http://gc.bcm.tmc.edu:8088/quality/info/genbank\\_annotation.html](http://gc.bcm.tmc.edu:8088/quality/info/genbank_annotation.html).

#### QUALSTAT-REPORT.

Location/Qualifiers

source

1..55001  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="12"  
/clone="RP11-568G5"  
1..11301  
/note="Overlaps bases 177088..178388 of clone AC079630"  
/function="clone overlap"

repeat\_region  
35..229  
/rpt\_family="MIR"  
repeat\_region  
1002..1023  
/rpt\_family="AT-rich"  
repeat\_region  
1092..1227  
/rpt\_family="MIR"  
repeat\_region  
complement(2156..2209)  
/rpt\_family="L2"  
repeat\_region  
3563..3650  
/rpt\_family="(CCGTA)n"  
repeat\_region  
complement(3688..3765)  
/rpt\_family="L2"  
repeat\_region  
complement(3840..3908)  
/rpt\_family="LIMD3"  
repeat\_region  
complement(4234..4464)  
/rpt\_family="MIR"  
repeat\_region  
complement(4847..4914)  
/rpt\_family="MIR"  
repeat\_region  
4938..5053  
/rpt\_family="L2"  
repeat\_region  
6350..6660  
/rpt\_family="AluSg"  
repeat\_region  
complement(7309..7743)  
/rpt\_family="L2"  
repeat\_region  
7744..9144  
/rpt\_family="L2P4"

repeat\_region complement(9151..9317)  
/rpt\_family="L2P4"  
repeat\_region 10587..10846  
/rpt\_family="L2P4"  
repeat\_region 10912..11015  
/rpt\_family="L2P4"  
repeat\_region 11098..11271  
/rpt\_family="L2P4"  
repeat\_region 11450..11635  
/rpt\_family="L2P4"  
repeat\_region 11941..12179  
/rpt\_family="MIR"  
repeat\_region 12797..12828  
/rpt\_family="(CATTAT)n"  
repeat\_region complement(12975..13087)  
/rpt\_family="L2P4"  
repeat\_region 13714..13737  
/rpt\_family="AT-rich"  
repeat\_region 14058..14219  
/rpt\_family="MIR45"  
repeat\_region 14411..14545  
/rpt\_family="MIR"  
repeat\_region complement(15058..15127)  
/rpt\_family="MIR"  
repeat\_region 16186..16413  
/rpt\_family="MIR"  
repeat\_region complement(17624..17922)  
/rpt\_family="AluB"  
repeat\_region complement(18309..18606)  
/rpt\_family="AluSx"  
repeat\_region 18844..18854  
/rpt\_family="AT-rich"  
repeat\_region complement(18855..19135)  
/rpt\_family="AluB"  
repeat\_region 19136..19158  
/rpt\_family="AT-rich"  
repeat\_region complement(20660..20753)  
/rpt\_family="MIR91C"  
repeat\_region 22179..22680  
/rpt\_family="(TAAA)n"  
repeat\_region 22180..22358  
/rpt\_family="AluB"  
repeat\_region 22359..22632  
/rpt\_family="AluB"  
repeat\_region 22633..22680  
/rpt\_family="(TAAA)n"  
repeat\_region 22682..22789  
/rpt\_family="AluB"  
repeat\_region 22796..23099  
/rpt\_family="AluY"  
repeat\_region complement(23147..23327)

Query Match 60.0%; Score 24; DB 8; Length 55001;  
Best Local Similarity 84.4%; Pred. No. 62;  
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

4 ATACTGCTCCCAACATCATCTCTCTCAT 35  
Db 47598 AACCTACTCCCAACATCATCTCTCAT 47567  
RESULT 14  
AL807784 127196 bp DNA linear ROD 13-NOV-2002  
LOCUS AL807784 Mouse DNA sequence from clone Rp23-448C18 on chromosome X, complete  
DEFINITION  
ACCESSION AL807784.11 GI:25045332  
VERSION  
KEYWORDS HTG.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus (house mouse);  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE 1 (bases 1 to 127196)  
 AUTHORS Howden, P.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 On Nov 15, 2002 this sequence version replaced gi:24939941.  
 Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk)

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-448C18 is from the RPCI-23 Mouse PAC library.

constructed by the group of Pieter de Jong.  
 For further details see <http://www.chori.org/bacpac/home.htm>

#### FEATURES

source  
 1..127196  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="X"  
 /clone="RP23-448C18"  
 /clone\_1ib="RPCI-23"

#### ORIGIN

Query Match 60.0%; Score 24; DB 9; Length 127196;  
 Best Local Similarity 75.0%; Pred.No. 55;  
 Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40  
 Db 110413 AGGATACATAAGCCAAATCACTTCTTACTAATGCCAC 110374

RESULT 15  
 AC157528 154857 bp DNA linear PRI 27-APR-2005  
 LOCUS Pan troglodytes BAC clone CH251-422M6 from chromosome unknown,  
 DEFINITION complete sequence.  
 AC157528  
 AC157528.2 GI:62000959  
 KEYWORDS HTG.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Pan.

REFERENCE 1 (bases 1 to 154857)  
 AUTHORS Shah, N., Cotton, M. and Lewis, S.  
 TITLE The sequence of Pan troglodytes BAC clone CH251-422M6  
 JOURNAL Unpublished (2001)  
 REFERENCE 2 (bases 1 to 154857)  
 AUTHORS Wilson, R.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-FEB-2005) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 3 (bases 1 to 154857)  
 AUTHORS Wilson, R.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-MAR-2005) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 154857)  
 AUTHORS Wilson, R.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-APR-2005) Washington University School of Medicine, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 154857)  
 AUTHORS Wilson, R.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-APR-2005) Washington University School of Medicine, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

#### COMMENT

----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu>  
 Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)

----- Summary Statistics  
 Center project name: C\_AB0422M06

#### NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
 Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

#### SOURCE INFORMATION:

The CHORI-251 Chimpanzee BAC library has been constructed at the Children's Hospital Oakland Research Institute, BACPAC Resources, by Dr. Baoji Zhu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, 'Cintu', Yerkes #C0471; birthdate:6-6-80). The clone and detailed information can be obtained from Pieter de Jong and co-workers at <http://www.bacpac.chori.org>.

#### FEATURES

source  
 1..154857  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /chromosome="unknown"  
 /clone="CH251-422M6"  
 /clone\_1ib="CHOR251"

This sequence is the entire insert of the clone.

unsure

unsure

unsure

#### ORIGIN

Query Match 60.0%; Score 24; DB 8; Length 154857;

Best Local Similarity 84.4%; Pred. No. 53;  
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 4 ATACTACTCCCAACAAATCCATCTTACTCAT 35  
Db 123632 AACTTACTCTCCCAACAAATCTTACTCAT 123663

Search completed: March 5, 2006, 21:55:48  
Job time : 176.689 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:08:23 ; Search time 26.619 Seconds  
(without alignments)

10014.946 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1239\_1278

Perfect score: 40  
Sequence: 1 aggaatacctactcccaaacatccattctactcatgcaac 40

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 333346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21.\*

1: geneseqn19808.\*  
2: geneseqn19808.\*  
3: geneseqn20008.\*  
4: geneseqn20018.\*  
5: geneseqn20018.\*  
6: geneseqn20018.\*  
7: geneseqn20028.\*  
8: geneseqn20038.\*  
9: geneseqn20038.\*  
10: geneseqn20038.\*  
11: geneseqn20038.\*  
12: geneseqn20048.\*  
13: geneseqn20048.\*  
14: geneseqn20058.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	40	5 AAH76337	Aah76337 Z. mays M
2	40	100.0	50	5 AAH76336	Aah76336 Z. mays M
3	40	100.0	158	5 AAH76334	Aah76334 Z. mays M
4	40	100.0	255	5 AAH76340	Aah76340 Z. mays M
5	40	100.0	1394	2 AAX07408	Aax07408 Zea mays
6	40	100.0	1394	2 AAX07409	Aax07409 Zea mays
7	40	100.0	1394	5 AAH76332	Aah76332 Z. mays M
8	40	100.0	1394	5 AAH76333	Aah76333 Z. mays M
9	30.4	76.0	2000	11 AC138730	Ac138730 Rice stre
10	22.4	56.0	226215	11 ACN45146	Acn45146 Human gen
11	21.6	54.0	4110	8 ABZ10202	Abz10202 Haematopo
12	21.6	54.0	6309	6 ABH33304	Abh33304 Human imm
13	21.6	54.0	7110	10 ADH84282	Adh84282 Pretreake
14	21.6	54.0	7110	10 ADH84196	Adh84196 Human lym
15	21.6	54.0	7110	13 ADH89580	Adh89580 Oligonuc
16	21.4	53.5	1341	6 ABZ13750	Abz13750 Arabidops
17	21.4	53.5	6681	6 ABZ13155	Abz13155 Human imm
18	21.4	53.5	6681	6 ABZ13155	Abz13155 Human imm
19	21.4	53.5	8168	6 ABZ132928	Abz132928 Human imm

C	20	21.4	53.5	8168	6 Aa633328	Aa633328 Chemical1
C	21	21.4	53.5	24401	4 AB103396	Ab103396 Drosophila
C	22	21	52.5	1531	14 ADW17938	Adw17938 Eucalyptu
C	23	21	52.5	2000	11 AC135665	Ac135665 Rice stre
C	24	21	52.5	2000	12 ADJ41594	Adj41594 Plant cDN
C	25	21	52.5	2792	12 ADM98941	Adm98941 Diterpene
C	26	21	52.5	3117	12 ADM98942	Adm98942 Diterpene
C	27	21	52.5	5507	8 ABZ10204	Abz10204 Haematopo
C	28	21	52.5	5507	8 ABZ10058	Abz10058 Haematopo
C	29	21	52.5	8404	4 Aa646500	Aa646500 Tumour su
C	30	21	52.5	8404	6 AB133595	Ab133595 Human imm
C	31	21	52.5	8404	10 ADB54216	Adb54216 Pretreake
C	32	21	52.5	8404	10 ADB54088	Adb54088 Pretreake
C	33	21	52.5	8404	10 ADB84076	Adb84076 Human lym
C	34	21	52.5	8404	10 ADB84152	Adb84152 Human lym
C	35	21	52.5	8404	13 ADB89586	Adb89586 Oligonuc
C	36	21	52.5	8404	4 Aa633308	Aa633308 Chemical1
C	37	21	52.5	10286	6 ABK28147	Abk28147 DNA trans
C	38	21	52.5	10286	6 ABK28147	Abk28147 DNA trans
C	39	21	52.5	63115	10 ADC85419	Adc85419 Mouse tile
C	40	21	52.5	63294	9 ADK02939	Adk02939 Mouse tile
C	41	21	52.5	63294	10 ADM72677	Adm72677 Mouse tile
C	42	21	52.5	63294	12 ADM74534	Adm74534 Murine ca
C	43	21	52.5	106315	11 ACN43966	Acn43966 Human gen
C	44	20.8	52.0	891	8 ABZ51893	Abz51893 Aspergill
C	45	20.8	52.0	6620	4 Aa645488	Aa645488 Chemical1

## ALIGNMENTS

RESULT 1  
ID AAH76337 standard; DNA; 40 BP.  
AC AAH76337;  
DT 29-OCT-2001 (first entry)  
DE Z. mays Ms45 male tissue-preferred regulatory region fragment.  
XX Ms45; male tissue; regulatory region; transcription; male fertility;  
XX hybrid seed; ds.  
XX Zea mays.  
XX OS  
XX WO200160997-A2.  
XX PD 23-AUG-2001.  
XX PF 13-FEB-2001; 2001MO-US004527.  
XX PR 15-FEB-2000; 2000US-00504487.  
XX PA (PION-) PIONEER HI-BRED INT INC.  
XX PI Albersen MC, Fox TW, Garnaat CW, Hufman G, Kendall TV,  
XX WPI; 2001-514772/56.  
XX DR A male tissue-preferred regulatory region comprising nucleotide sequences  
XX essential for initiating transcription of the Ms45 gene useful for  
XX mediating fertility in a male plant.  
XX PT  
XX Claim 14; Page 32; 50pp; English.  
XX PS  
XX The invention provides a male tissue-preferred regulatory region (i)  
XX comprising nucleotide sequences essential for initiating transcription of  
XX the Ms45 gene. A method of mediating male fertility in a plant is  
XX provided that involves introducing an expression vector comprising a  
XX promoter operably linked to (i) into a plant where the exogenous gene  
XX impacts male fertility of the plant and (i) controls expression of the  
XX exogenous gene. A method of producing hybrid seeds is also provided. The

CC present sequence represents a DNA fragment upstream of the TATA box of a  
CC Z. mays Ms45 male-tissue preferred regulatory region nucleotide sequence  
XX  
SQ Sequence 40 BP; 14 A; 14 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 40; DB 5; Length 40;  
Best Local Similarity 100.0%; Pred. No. 4.1e-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40  
DB 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40

## RESULT 2

AAH76336  
ID AAH76336 standard; DNA; 50 BP.

AAH76336;

DT 29-OCT-2001 (first entry)

DE Z. mays Ms45 male tissue-preferred regulatory region fragment.

XX Ms45; male tissue; regulatory region; transcription; male fertility;

KM hybrid seed; ds.

XX Zea mays.

PN WO200160997-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001WO-US004527.

XX 15-FEB-2000; 2000US-00504487.

XX (PION-) PIONEER HI-BRED INT INC.

PI Albersen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;

XX WPI; 2001-514772/56.

PT A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the Ms45 gene useful for  
PT mediating fertility in a male plant.

XX Claim 5; Page 47; 50pp; English.

CC The invention provides a male tissue-preferred regulatory region (I)  
CC comprising nucleotide sequences essential for initiating transcription of  
CC the Ms45 gene. A method of mediating male fertility in a plant is  
CC provided that involves introducing an expression vector comprising a  
CC promoter operably linked to (i) into a plant where the exogenous gene  
CC impacts male fertility of the plant and (i) controls expression of the  
CC exogenous gene. A method of producing hybrid seeds is also provided. The  
CC present sequence represents a DNA fragment -72 to -111 bases upstream of  
CC the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region  
CC nucleotide sequence

XX Sequence 50 BP; 18 A; 17 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 40; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40  
DB 11 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 50

RESULT 3  
AAH76334

ID AAH76334 standard; DNA; 158 BP.

AAH76334;

DT 29-OCT-2001 (first entry)

DE Z. mays Ms45 male tissue-preferred regulatory region fragment.

XX Ms45; male tissue; regulatory region; transcription; male fertility;

KM hybrid seed; ds.

XX Zea mays.

PN WO200160997-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001WO-US004527.

XX 15-FEB-2000; 2000US-00504487.

XX (PION-) PIONEER HI-BRED INT INC.

PI Albersen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;

XX WPI; 2001-514772/56.

PT A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the Ms45 gene useful for  
PT mediating fertility in a male plant.

XX Claim 5; Page 47; 50pp; English.

CC The invention provides a male tissue-preferred regulatory region (I)  
CC comprising nucleotide sequences essential for initiating transcription of  
CC the Ms45 gene. A method of mediating male fertility in a plant is  
CC provided that involves introducing an expression vector comprising a  
CC promoter operably linked to (i) into a plant where the exogenous gene  
CC impacts male fertility of the plant and (i) controls expression of the  
CC exogenous gene. A method of producing hybrid seeds is also provided. The  
CC present sequence represents a DNA fragment -18 to -195 bases upstream of  
CC the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region  
CC nucleotide sequence

XX Sequence 158 BP; 41 A; 50 C; 21 G; 46 T; 0 U; 0 Other;

Query Match 100.0%; Score 40; DB 5; Length 158;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40  
DB 86 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 125

RESULT 4  
AAH76340  
ID AAH76340 standard; DNA; 255 BP.

AAH76340;

DT 29-OCT-2001 (first entry)

DE Z. mays Ms45 promoter fragment.

XX Ms45; male tissue; regulatory region; transcription; male fertility;

KM hybrid seed; promoter; ds.

XX Zea mays.

PN WO200160997-A2.

PD 23-AUG-2001.

XX 13-FEB-2001; 2001WO-US004527.  
 XX 15-FEB-2000; 2000US-00504487.  
 XX (PION-) PIONEER HI-BRED INT INC.  
 PA  
 PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;  
 XX WPI; 2001-514772/56.  
 DR  
 XX A male tissue-preferred regulatory region comprising nucleotide sequences  
 PT essential for initiating transcription of the Ms45 gene useful for  
 PT mediating fertility in a male plant.  
 XX  
 XX Example 5; Fig 8; 50pp; English.  
 XX The invention provides a male tissue-preferred regulatory region (I)  
 CC comprising nucleotide sequences essential for initiating transcription of  
 CC the Ms45 gene. A method of mediating male fertility in a plant is  
 CC provided that involves introducing an expression vector comprising a  
 CC promoter operably linked to (I) into a plant where the exogenous gene  
 CC impacts male fertility of the plant and (I) controls expression of the  
 CC exogenous gene. A method of producing hybrid seeds is also provided. The  
 CC present sequence represents a Z. mays Ms45 promoter fragment  
 XX  
 SO Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 40; DB 5; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGGATACCTACTCCCAACATCCATCTTACTGACGAC 40  
 DB 99 AGGATACCTACTCCCAACATCCATCTTACTGACGAC 138  
 RESULT 5  
 ID AAX07408 standard; DNA; 1394 BP.  
 XX  
 AC AAX07408;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Zea mays Ms45 male tissue-preferred regulatory region.  
 XX  
 KM Ms45; male; tissue-preferred; regulatory region; plant cells;  
 KM plant tissue; differentiated; maize; hybrid seed; fertility; ss.  
 OS  
 OS Zea mays.  
 OS  
 PN WO9859061-A1.  
 XX  
 PD 30-DEC-1998.  
 XX  
 PF 19-JUN-1998; 98WO-US012895.  
 XX  
 PR 23-JUN-1997; 97US-00880499.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL;  
 XX WPI; 1999-105628/09.  
 DR  
 XX New nucleic acid encoding a Ms45 male tissue-preferred regulatory region  
 PT - useful in mediating plant fertility, especially hybrid seed production.  
 XX  
 XX Claim 2; Page 22-23; 39pp; English.  
 XX The sequence is that encoding an Ms45 male tissue-preferred regulatory  
 CC region. It may be used in the construction of a vector for a method of

CC producing exogenous genes in a male tissue-preferred manner, which is  
 CC useful in restoring or conferring fertility, such as in hybrid seed  
 CC production. In conferring fertility a monocot/dicot plant is transformed  
 CC with the exogenous nucleotide sequence (a male sterility gene, preferably  
 CC Ms45), which encodes a product selected from auxins, rolB and diphenyl  
 CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile  
 CC and infertile plants  
 XX  
 SO Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 40; DB 2; Length 1394;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGGATACCTACTCCCAACATCCATCTTACTGACGAC 40  
 DB 1239 AGGATACCTACTCCCAACATCCATCTTACTGACGAC 1278  
 RESULT 6  
 ID AAX07409 standard; DNA; 1394 BP.  
 XX  
 AC AAX07409;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Zea mays Ms45 male tissue-preferred regulatory region.  
 XX  
 KM Ms45; male; tissue-preferred; regulatory region; plant cells;  
 KM plant tissue; differentiated; hybrid seed; fertility; ss.  
 OS  
 OS Zea mays.  
 OS  
 PN WO9859061-A1.  
 XX  
 PD 30-DEC-1998.  
 XX  
 PF 19-JUN-1998; 98WO-US012895.  
 XX  
 PR 23-JUN-1997; 97US-00880499.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL;  
 XX WPI; 1999-105628/09.  
 DR  
 XX New nucleic acid encoding a Ms45 male tissue-preferred regulatory region  
 PT - useful in mediating plant fertility, especially hybrid seed production.  
 XX  
 XX Claim 3; Page 23-24; 39pp; English.  
 XX The sequence is that encoding an Ms45 male tissue-preferred regulatory  
 CC region. It may be used in the construction of a vector for a method of  
 CC producing exogenous genes in a male tissue-preferred manner, which is  
 CC useful in restoring or conferring fertility, such as in hybrid seed  
 CC production. In conferring fertility, a monocot/dicot plant is transformed  
 CC with the exogenous nucleotide sequence (a male sterility gene, preferably  
 CC Ms45), which encodes a product selected from auxins, rolB and diphenyl  
 CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile  
 CC and infertile plants  
 XX  
 SO Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 40; DB 2; Length 1394;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGGATACCTACTCCCAACATCCATCTTACTGACGAC 40  
 DB 1239 AGGATACCTACTCCCAACATCCATCTTACTGACGAC 1278

```
RESULT 7
AAH76332 standard; DNA; 1394 BP.
AC AAH76332;
XX
XX 29-OCT-2001 (first entry)
DT
XX
XX Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
DE
XX Ms45; male tissue; regulatory region; transcription; male fertility;
KM hybrid seed; ds.
XX
XX Zea mays.
OS
XX MO200160997-A2.
PN
XX 23-AUG-2001.
PD
XX 13-FEB-2001; 2001WO-US004527.
PF
XX 15-FEB-2000; 2000US-00504487.
PR
XX (PION-) PIONEER HI-BRED INT INC.
PA
XX
XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
PI WPI; 2001-514772/56.
DR
XX
XX A male tissue-preferred regulatory region comprising nucleotide sequences
PT essential for initiating transcription of the MS45 gene useful for
PT mediating fertility in a male plant.
XX
XX Claim 4; Page 46; 50pp; English.
PS
XX The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription of
CC the MS45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided. The
CC present sequence represents a nucleic acid sequence encoding an Ms45 male
CC tissue preferred regulatory region from Z. mays
CC
XX
SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
Query Match 100.0%; Score 40; DB 5; Length 1394;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGGATCTACTCTCCCAACATCCATCTTACTCATGCAC 40
DB 1239 AGGATCTACTCTCCCAACATCCATCTTACTCATGCAC 1278
RESULT 8
AAH76333
ID AAH76333 standard; DNA; 1394 BP.
XX
XX AAH76333;
AC
XX 29-OCT-2001 (first entry)
DT
XX
XX Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
DE
XX Ms45; male tissue; regulatory region; transcription; male fertility;
KM hybrid seed; ds.
XX
XX Zea mays.
OS
XX MO200160997-A2.
PN
```

```
XX
XX 23-AUG-2001.
PD
XX
XX 13-FEB-2001; 2001WO-US004527.
PF
XX 15-FEB-2000; 2000US-00504487.
PR
XX (PION-) PIONEER HI-BRED INT INC.
PA
XX
XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
PI WPI; 2001-514772/56.
DR
XX
XX A male tissue-preferred regulatory region comprising nucleotide sequences
PT essential for initiating transcription of the MS45 gene useful for
PT mediating fertility in a male plant.
XX
XX Claim 4; Page 47; 50pp; English.
PS
XX The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription of
CC the MS45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided. The
CC present sequence represents a nucleic acid sequence encoding an Ms45 male
CC tissue preferred regulatory region from Z. mays
CC
XX
SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
Query Match 100.0%; Score 40; DB 5; Length 1394;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGGATCTACTCTCCCAACATCCATCTTACTCATGCAC 40
DB 1239 AGGATCTACTCTCCCAACATCCATCTTACTCATGCAC 1278
RESULT 9
ACL38730
ID ACL38730 standard; cDNA; 2000 BP.
XX
XX ACL38730;
AC
XX 02-JUN-2005 (first entry)
DT
XX
XX Rice stress-regulated promoter SBQ ID NO:17293.
DE
XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KM agriculture.
XX
XX Oryza sativa.
OS
XX
XX MO2003008540-A2.
PN
XX 30-JAN-2003.
PD
XX 21-JUN-2002; 2002WO-US019668.
PF
XX 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Kieps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Rieke D, Zhu T;
XX WPI; 2003-248011/24.
DR
XX
```

PT New stress-responsive nucleic acid, useful for altering the  
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
 PT stress, salt stress or osmotic stress.  
 PS Claim 48; SEQ ID NO 17293; 89pp; English.  
 CC The invention relates to novel abiotic stress responsive polynucleotides  
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
 CC cells, and plants containing such polynucleotides. Also disclosed are  
 CC methods for using the polynucleotides and polypeptides to alter the  
 CC responsiveness of a plant to abiotic stress. The invention is useful in  
 CC agriculture. The nucleic acid is useful for determining whether a test  
 CC plant has been exposed to an abiotic stress condition. It is also useful  
 CC for selecting an agent that alters abiotic stress regulated  
 CC polynucleotide expression in a plant cell, and to identify a homolog or  
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
 CC molecule and the polypeptide encoded by it are useful in altering the  
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
 CC stress, osmotic stress or any of their combinations. The present sequence  
 CC is used in the exemplification of the invention  
 SO Sequence 2000 BP; 616 A; 370 C; 355 G; 659 T; 0 U; 0 Other;  
 QY Query Match 76.0%; Score 30.4; DB 11; Length 2000;  
 Best Local Similarity 85.0%; Pred. No. 0.047;  
 Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 DB 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40  
 1840 AGAACACCTACTCCCAACATCAACGCTGACTCATGCAAC 1879  
 RESULT 10  
 ID ACN45146 standard; DNA; 226215 BP.  
 AC ACN45146;  
 DT 18-NOV-2004 (first entry)  
 XX Human genomic sequence hCG1639824.  
 DE  
 KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.  
 OS Homo sapiens.  
 PN WO2003073826-A2.  
 XX  
 PD 12-SEP-2003.  
 XX  
 PF 28-FEB-2003; 2003WO-US006235.  
 XX  
 PR 01-MAR-2002; 2002US-00087192.  
 XX  
 PA (SAGR-) SAGRES DISCOVERY.  
 XX  
 PI Morris DW;  
 XX  
 DR WPI; 2003-328604/31.  
 XX  
 PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma  
 PT comprises a nucleotide sequence.  
 PS Claim 1; SEQ ID NO 1948; 0pp; English.  
 CC The present invention relates to novel DNA and protein sequences which  
 CC are associated with carcinomas. The sequences are useful for: (i) for  
 CC screening drug candidates; (ii) for screening of bioactive agent capable  
 CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of  
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for  
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing  
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating  
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;

CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for  
 CC determining Carcinoma Associated (CA) gene copy number. In addition, the  
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of  
 CC carcinoma including lymphoma. The present sequence is one such CA coding  
 CC sequence. Note: This patent is an equivalent to basic patent  
 CC US2002182586A1, for which no sequence data was published  
 CC  
 SO Sequence 226215 BP; 65331 A; 42804 C; 45218 G; 72862 T; 0 U; 0 Other;  
 QY Query Match 56.0%; Score 22.4; DB 11; Length 226215;  
 Best Local Similarity 72.5%; Pred. No. 1.4e+02;  
 Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 DB 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40  
 183206 AGAATTCCTGCTCCCAACATCAACGATCTTACTCTTTAC 183245  
 RESULT 11  
 ID ABZ10202/c  
 ABZ10202 standard; DNA; 4110 BP.  
 AC ABZ10202;  
 DT 16-JAN-2003 (first entry)  
 XX  
 DE Haematopoietic cell proliferation disorder related DNA sequence #342.  
 XX  
 KW Human, haematopoietic cell proliferation disorder; cytostatic;  
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
 KW cytosine methylation state; gene; ds.  
 OS Homo sapiens.  
 PN WO200277272-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-EP003401.  
 XX  
 PR 26-MAR-2001; 2001US-0278333P.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Berlin K, Braun A, Dietler J, Gnetig D, Howe A, Mueller J;  
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
 PI Schwabe I, Ziebarth H;  
 XX  
 DR WPI; 2003-018942/01.  
 XX  
 PT Detecting and differentiating between hematopoietic cell proliferative  
 PT disorders, comprises contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.  
 PS Claim 28; SEQ ID NO 342; 117pp; English.  
 CC The present invention describes a method for detecting and  
 CC differentiating between hematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used; for  
 CC differentiating between healthy hematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA

CC sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between CC subtypes, diagnosis, prognosis, treatment and/or monitoring of CC hemotopietic cell proliferative disorders. The present method enables a highly specific classification of hemotopietic cell proliferative disorders allowing for improved and informed treatment of patients

CC Sequence 4110 BP; 945 A; 0 C; 1132 G; 2033 T; 0 U; 0 Other;

Query Match 54.0%; Score 21.6; DB 8; Length 4110;

Best Local Similarity 85.7%; Pred. No. 1.6e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ATACTACTCCCAACATCATCTTAC 31

Db 3083 AACCTAACCCCAACATCATCTTAC 3056

RESULT 12 ABL32304/c

ID ABL32304 standard; DNA; 6309 BP.

XX ABL32304;

XX 26-MAR-2002 (first entry)

DE Human immune system associated gene SEQ ID NO: 277.

XX Human; immune system disease; cytosine methylation; antiasthmatic;  
KM antiasthmatic; antiasthmatic; antiasthmatic; antiasthmatic;  
KM neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
KM antineoplastic; antineoplastic; antidiabetic; antiproliferative;  
KM antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;  
KM acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
KM neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;  
ds.

XX Homo sapiens.

XX W0200200928-A2.

XX 03-JAN-2002.

PF 02-JUL-2001; 2001WO-EP007537.

XX 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-130909/17.

PT Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.

PS Claim 1; SEQ ID NO 277; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated CC genes which are modified by the methylation of cytosines. The sequences CC can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention

XX Sequence 6309 BP; 1758 A; 69 C; 1364 G; 3118 T; 0 U; 0 Other;

Query Match 54.0%; Score 21.6; DB 6; Length 6309;

Best Local Similarity 75.0%; Pred. No. 1.7e+02;

Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ATACTACTCCCAACATCATCTTAC 39

Db 3335 ATACTACTCCCAACATCATCTTAC 3300

RESULT 13

ID ADB54282/c

XX ADB54282 standard; DNA; 7110 BP.

XX ADB54282;

XX 04-DEC-2003 (first entry)

DE Pretreated genomic DNA region 206.

XX colon cell proliferative disorder; non methylated CpG dinucleotide;  
KM cytosine methylation state; ds.

XX Unidentified.

XX W02003072821-A2.

XX 04-SEP-2003.

PF 27-FEB-2003; 2003WO-EP002035.

XX 27-FEB-2002; 2002EP-00004551.

XX (EPIG-) EPIGENOMICS AG.

PI Adorjan P, Burger M, Maier S, Nimrich I, Becker E, Lesche R;

PI Rujan T, Schmitt A;

XX WPI; 2003-731620/69.

PT Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with a reagent.

PS Claim 32; SEQ ID NO 338; 74pp; English.

XX The invention relates to a novel method for detecting and differentiating CC between colon cell proliferative disorders associated with at least one CC gene or its regulatory regions. The method comprises contacting a target CC nucleic acid in a biological sample obtained from the subject with at least one reagent or a series of reagents, where the reagent or series of reagents, distinguishes between methylated and non methylated CpG dinucleotides within the target nucleic acid. The molecules of the CC invention demonstrate cytosine methylation activity whilst the method useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenoma and colon carcinoma. CC The PNA (peptide nucleic acid)-oligonucleotides are useful as probes for CC determining cytosine methylation state or single nucleotide CC polymorphisms. The current sequence is that of the pretreated genomic DNA CC region of the invention. This sequence is not shown within the CC specification but is taken from Wipoweb.

XX Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;

Query Match 54.0%; Score 21.6; DB 10; Length 7110;

Best Local Similarity 85.7%; Pred. No. 1.7e+02; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ATACTACTCCCAACATCATCTTAC 31

Db 3083 AACCTAACCCCAACATCATCTTAC 3056

RESULT 14

ADBE84196/c

ID ADE84196 standard; DNA; 7110 BP.  
 AC ADE84196;  
 XX  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human lymphoid cell proliferative disorder gene derived DNA #133.  
 XX  
 KW de; lymphoid cell proliferative disorder; methylation;  
 KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;  
 KW diffuse large B-cell lymphoma; mantle cell lymphoma;  
 KW chronic lymphocytic leukemia; small lymphocytic lymphoma;  
 KW follicular lymphoma; diagnosis; prognosis.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO2003044226-A2.  
 XX  
 PD 30-MAY-2003.  
 XX  
 PF 25-NOV-2002; 2002WO-EP013365.  
 XX  
 PR 23-NOV-2001; 2001DE-01057491.  
 XX  
 PR 28-DEC-2001; 2001DE-01064501.  
 XX  
 PA (EPIC-) EPIDENOMICS AG.  
 XX  
 PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;  
 XX  
 DR WPI; 2003-457621/43.  
 XX  
 PT Detecting and differentiating between lymphoid cell proliferative  
 PT disorder comprising contacting a target nucleic acid with at least one  
 PT reagent that distinguishes between methylated and non-methylated CpG  
 PT dinucleotides.  
 XX  
 PS Claim 26; SEQ ID NO 192; 448bp; English.  
 XX  
 CC The invention relates to a method of detecting and differentiating  
 CC between lymphoid cell proliferative disorders associated with at least  
 CC one gene and/or their regulatory regions in a subject by contacting a  
 CC target nucleic acid in a biological sample obtained from the subject with  
 CC at least one reagent or series of reagents that distinguish between  
 CC methylated and non-methylated CpG dinucleotides within the target nucleic  
 CC acid. The genes and/or their regulatory regions are preferably selected  
 CC from MDR1, CSNK2B, BGR4, AR, CDK4, RB2, CDC25A, GPR beta, MYO1, CDH3,  
 CC MYC1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2A, CDKN2B, FOS,  
 CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB2, TGFBR2, TP73, CDKN1C,  
 CC GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic  
 CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences  
 CC of the genes are useful for detecting the methylation state of all the  
 CC CpG dinucleotides within one or more the sequences, or their complements,  
 CC for determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) and for differentiating at least two of the medical  
 CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,  
 CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular  
 CC lymphoma. They are also useful for detecting of a predisposition to,  
 CC differentiation between subclasses, diagnosis, prognosis, treating and/or  
 CC monitoring of lymphoid cell proliferative disorder. This sequence  
 CC represents a nucleic acid of a pretreated genomic DNA derived from the  
 CC above mentioned genes.  
 XX  
 SQ Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;  
 XX  
 QY Query Match 54.0%; Score 21.6; DB 10; Length 7110;  
 XX  
 XX Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
 XX  
 XX Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 DB 4 ATACTACTCCCAACATCATCTTAC 31  
 DB 3083 AACCTTAACCCCAACATCATCTTAC 3056

RESULT 15  
 ID ADS89580/c  
 ID ADS89580 standard; DNA; 7110 BP.  
 AC ADS89580;  
 XX  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Oligonucleotide of the invention SEQ ID NO:596.  
 XX  
 KW ss; cell proliferative disorder; breast; methylation; cytostatic;  
 KW gene therapy; single nucleotide polymorphism; SNP.  
 XX  
 OS Unidentified.  
 XX  
 EN WO2004035803-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PF 01-OCT-2003; 2003WO-EP010881.  
 XX  
 PR 01-OCT-2002; 2002DE-01045779.  
 XX  
 PR 07-JAN-2003; 2003DE-0100096.  
 XX  
 PR 17-APR-2003; 2003DE-01017955.  
 XX  
 PA (EPIC-) EPIDENOMICS AG.  
 XX  
 PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;  
 XX  
 PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;  
 XX  
 DR WPI; 2004-348468/32.  
 XX  
 PT Predicting responsiveness of a subject with breast cell proliferative  
 PT disorder, useful for treating or differentiating breast cell  
 PT proliferative disorders comprising analyzing methylation pattern of a  
 PT genomic DNA from the subject.  
 XX  
 PS Disclosure; SEQ ID NO 596; 104bp; English.  
 XX  
 CC The invention relates to a novel method for predicting the responsiveness  
 CC of a subject with a cell proliferative disorder of the breast tissues to  
 CC a therapy comprising analysing the methylation pattern of a target  
 CC nucleic acid by contacting at least one of the target nucleic acids in a  
 CC biological sample obtained from the subject prior to or during treatment.  
 CC The method of the invention has cytostatic activity, and may have a use  
 CC in gene therapy. The set of oligonucleotides comprising at least two of  
 CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The  
 CC method, nucleic acid, oligonucleotide, and kit are useful for the  
 CC treatment, characterization, classification and/or differentiation, of  
 CC breast cell proliferative disorders. The method is also useful for  
 CC predicting the responsiveness of a subject with a cell proliferative  
 CC disorder of the breast tissues to a therapy. The present sequence is used  
 CC in the exemplification of the invention.  
 XX  
 SQ Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;  
 XX  
 QY Query Match 54.0%; Score 21.6; DB 13; Length 7110;  
 XX  
 XX Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
 XX  
 XX Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 DB 4 ATACTACTCCCAACATCATCTTAC 31  
 DB 3083 AACCTTAACCCCAACATCATCTTAC 3056  
 XX  
 XX Search completed: March 5, 2006, 18:11:42  
 XX  
 XX Job time : 26.619 secs

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## SUMMARIES

```

Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TP

FEATURES
    source
        1..687
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="mp73"
            /BD_xref="tixon:4577"
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            /clone_id="ZM_0.7-1.5 kb"
            /note="Vector: pGCS+; Site 1, HincII; 0.7-1.5 kb
            methylation filtered genomic DNA library"

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Best Local Similarity 100.0%; Prid. No. 4e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGGATACCTACTCCCAACAAATCCATCTTACTACATGCAAC 40

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C	23	22.6	56.5	630	9	BZ173301	BZ173201	CH230-369
C	24	22.6	56.5	644	11	CR843905	CR843905	CR00AA79A
C	25	22.6	56.5	664	9	AZ400686	AZ400686	IM0167P01
C	26	22.6	56.5	691	1	AM687128	AM687128	IN006C08R
C	27	22.6	56.5	706	11	CR811830	CR811830	GR04AA43D
C	28	22.6	56.5	1080	10	CL058859	CL058859	CH216-88P
C	29	22.4	56.0	298	8	BB264116	BB264116	BB264116
C	30	22.4	56.0	804	8	D7054853	D7054853	AGENCOURT
C	31	22.4	56.0	940	7	CR664514	CR664514	AGENCOURT
C	32	22.4	56.0	940	7	CR671857	CR671857	AGENCOURT
C	33	22.4	56.0	951	7	CN171330	CN171330	AGENCOURT
C	34	22.2	55.5	273	1	AI106216	AI106216	Q27F06.x
C	35	22.2	55.5	346	1	AI698201	AI698201	wa67G01.x
C	36	22.2	55.5	398	1	AA725064	AA725064	wa67G07.s
C	37	22.2	55.5	417	1	AI647879	AI647879	tc378e09.x
C	38	22.2	55.5	479	2	BF601210	BF601210	266128.MA
C	39	22.2	55.5	491	1	AI182034	AI182034	tc333g05.x
C	40	22.2	55.5	609	3	BM027586	BM027586	CIT000109
C	41	22.2	55.5	727	7	CK949745	CK949745	407949.6
C	42	22.2	55.5	802	10	CG811817	CG811817	FSMA5518R
C	43	22.2	55.5	874	10	CG727957	CG727957	OC.BA005
C	44	22.2	55.5	940	10	CG383910	CG383910	AGAP61TV
C	45	22.2	55.5	1090	10	CL084441	CL084441	ISB1-3G16

## ALIGNMENTS

```

RESULT 1
LOCUS CC656939/c
DEFINITION OGMQ20YTM 2M 0.7-1.5 KB Zea mays genomic clone ZM6BA054D15,
genomic survey sequence.
ACCESSION CC656939
VERSION CC656939.1 GI:32060231
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Pooideae;
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 687)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Frazer,C.M., Buddiman,W.A., Betzell,J.A., Rohlfing,T.,
Citek,R.W., Nunez,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGMQ20YTM
Contact: Cathy WhiteLaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5883
Fax: 301-838-0208
Email: whiteLaw@cbl.tigr.org
Seq primer: T
Class: methylation filtered.
Location/Qualifiers
1..687
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM6BA054D15"
/clone_1lb="ZM 0.7-1.5 KB"
/note="Vector: pBCKR; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 100.0%; Score 40; DB 9; Length 687;
Best Local Similarity 100.0%; Pred.No. 4e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGGATCACTACTCCCAACAAATCACTTACTCATGCAC 40

```

Db 337 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 298

RESULT 2	CG224225	LOCUS	DEFINITION
	CG224225	915 bp	DNA
	CGIAG08TV ZM 0.7_1.5_KB	Zea mays	genomic clone ZMMBMA0716B15,
			genomic survey sequence.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 915)	Whitehead C.A., Quackenbush, J., Van Aken, S., Uterrecher, T.,			
	Clenck R.A., Fraser C.M., Budiman, M.A., Bedell J.A., Rohling, T.,			
	Reick R.W., Numborg, A., Robbins, D. and Lakey, N.			
	Consortium for Maize Genomics			
	Unpublished (2002)			
	Other_GSSs: OGIAG087H			

### FEATURES

Location/Qualifiers

## ORIGIN

Query Match	100.0%	Score 40	DB 10	Length 915
Best Local Similarity	100.0%	Pred. No. 4.2e-05		
Matches 40	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	AGGATACCTACTCCGAACCAATCCATCTTTATCATGCAAC	40	
Db	618	AGGATACCTACTCCGAACCAATCCATCTTTATCATGCAAC	657	

RESULT_3					
CC656933					
LOCUS	CC656933	963 bp	DNA	linear	GSS 19-JUN-2003
DEFINITION	OCNDQ2OTM_ZM_0.7.1.5_KB_Zea mays genomic clone ZMMBMA054D15,				
	genomic survey sequence.				
ACCESSION	CC656933				
VERSION	CC656933.1	GI:32060225			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 963)	Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Reenick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Konifong, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.	Consortium for Maize Genomics	Unpublished (2002)	Other_GSSs: GMDQ20TV

Contact: Cathy Whitelaw  
TIGR

## ORIGIN

	Query Match	100.0%	Score 40	DB 9	Length 963
	Best Local Similarity	100.0%	Pred. No.	4.2e-05	
	Matches	40;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
Qy	1 AGGATACCTACTCCCAAAACATCGATTACTTCGAC	40			
Db	836 AGGATACCTACTCCCAAAACATCGATTACTTCGAC	875			

RESULT 4	CM324514	LOCUS	DEFINITION
	CM324514	702 bp	DNA linear
	104 819 11477203	148 35910 078	Sorghum methylation filtered library (libID: 104) Sorghum bicolor genomic clone 11477203, genomic survey sequence.

FEATURES	Location/Qualifiers
source	1. .702

## ORIGIN

Query Match 88.0%; Score 35.2; DB 10; Length 702;  
 Best Local Similarity 92.5%; Pred. No. 0.0034;  
 Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

end-repaired, size fractionated to enrich for the 0.5 to 5  
 kb fraction, ligated into HincII-digested pBCK(-) vector  
 and electroporated into E. coli cells. This is a  
 methylation filtered library."

Db 1 AGGATGACCTACTCCCAACATCTCTTCATCCATCCAC 40  
 74 AGGACACCTACTCCCAACATCTCTTCATCCATCCAC 113

## RESULT 5

## LOCUS

CM445575 296 bp DNA linear GSS 02-NOV-2004  
 Definition Sorghum bicolor genomic clone fdbb001f170m16, genomic survey

Accession CM445575.1 GI:55193536  
 Version CM445575.1  
 Keywords Sorghum bicolor (sorghum)

Source Sorghum bicolor (sorghum)  
 Organism Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD  
 clade; Panicoideae; Andropogoneae; Sorghum.

## REFERENCE

## AUTHORS

Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
 Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,  
 McMenamy, J., Smith, M., Holman, H., Roe, B.A., Wiley, G., Korf, I.F.,  
 Robinson, J., D., Lakey, N., McCombie, W.R., Jedd, J., A. and  
 Martensen, R.A.  
 Sorghum genome sequencing by methylation filtration  
 PLoS Biol. 3 (1), e13 (2005)  
 15660154

## COMMENT

Contact: Bedell JA  
 Orion Genomics, LLC  
 4041 Forest Park Ave., St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@oriongenomics.com  
 Plate: fdbb001f170 row: m column: 16  
 Seq primer: K Reverse  
 Class: methylation filtered  
 High quality sequence stop: 296.  
 Location/Qualifiers

## FEATURES

## source

1..296  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /cultivar="Rix823"  
 /db\_xref="taxon:4558"  
 /clone="fdbb001f170m16"  
 /clone\_lib="Sorghum methylation filtered library (libid:  
 104)"  
 /note="Organ: leaf; Vector: pBCK(-); Site 1: HincII; DNA  
 prepared from purified nuclei was randomly sheared,  
 end-repaired, size fractionated to enrich for the 0.5 to 5  
 kb fraction, ligated into HincII-digested pBCK(-) vector  
 and electroporated into E. coli cells. This is a  
 methylation filtered library."

## ORIGIN

Query Match 60.5%; Score 24.2; DB 10; Length 296;  
 Best Local Similarity 90.2%; Pred. No. 75;  
 Matches 37; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Db 1 AGGATGACCTACTCCCAACATCTCTTCATCCATCCAC 40  
 242 AGGACACCTACTCCCAACATCTCTTCATCCATCCAC 282

## RESULT 6

## LOCUS

H24137 528 bp mRNA linear EST 06-JUL-1995  
 Definition U05008.1 Soares infant brain INIB Homo sapiens cDNA clone  
 IMAGE:51939 5', mRNA sequence.

Accession H24137.1 GI:892832  
 Version H24137.1  
 Keywords EST.  
 Source Homo sapiens (human)  
 Organism Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

## REFERENCE

## AUTHORS

1 (bases 1 to 528)  
 Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.  
 The Mashu-Merck EST Project  
 Unpublished (1995)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1161  
 High quality sequence stops: 349  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 1161 Std Error: 0.00  
 Seq primer: M13RPI  
 High quality sequence stop: 349.  
 Location/Qualifiers

## FEATURES

## source

1..528  
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 /db\_xref="taxon:9606"  
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 /sex="female"  
 /dev\_stage="73 days post natal"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares infant brain INIB"  
 /note="Organ: whole brain; Vector: Latmid BA; Site 1: Not  
 I; Site 2: Hind III; 1st strand cDNA was primed with a Not  
 I - oligo(dT) primer [5'  
 AACTGAGAAATTCGCGCGCGAGGAAATTTTCTTTTCTTTT 3'];  
 double-stranded cDNA was ligated to Hind III adaptors  
 (Pharmacia), digested with Not I and directionally cloned  
 into the Not I and Hind III sites of the Latmid BA vector.  
 Library went through one round of normalization. Library  
 constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 59.5%; Score 23.8; DB 8; Length 528;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 4 AATCTACTCTCAACATCTCTTCATCCATCCAC 38  
 346 AATCTACTCTCAACATCTCTTCATCCATCCAC 380

## RESULT 7

## LOCUS

B2706605/c 375 bp DNA linear GSS 18-MAY-2003  
 Definition SM41681-007.55.13.ab1 Spider Monkey genomic BAC library Ateles  
 Geoffroyi genomic, genomic survey sequence.  
 Accession B2706605

VERSION B2706605.1 GI:30843142  
KEYWORDS GSS.  
SOURCE Ateles Geoffroyi (black-handed spider monkey)  
ORGANISM Ateles geoffroyi  
REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;  
Cebidae; Ateleinae; Ateles.  
1 (bases 1 to 375)  
Qian, Y., Jin, L., and Su, B.  
TITLE Construction and characterization of bacterial artificial  
chromosome library of black-handed spider monkey (Ateles geoffroyi)  
JOURNAL Genome 47 (2), 239-245 (2004)  
PUBMED 15060576  
COMMENT Contact: Qian Y, Jin L, Su B.  
Center for Genome Information  
University of Cincinnati  
Kettering Lab, 3223 Eden Ave., Cincinnati, OH 45267-0056, USA  
Tel: 1-513-558-6678  
Fax: 1-513-558-4505  
Email: subnuc@mail.uc.edu  
Seq primer: T7  
Class: BAC ends.

FEATURES  
source  
1..375  
/organism="Ateles geoffroyi"  
/mol\_type="genomic DNA"  
/strain="black-handed spider monkey"  
/db\_xref="taxon:9509"  
/sex="Male"  
/tissue\_type="Skin"  
/cell\_type="Fibroblast"  
/cell\_line="AG05352"  
/dev\_stage="3 DA"  
/clone\_lib="Spider Monkey genomic BAC library"  
/note="Vector: pBAC3.6; Site 1: EcoRI; Genomic DNA was  
partially digested with EcoRI; Vector: pBAC3.6.  
Recombinants were transformed into DH10B."

ORIGIN  
Query Match 59.0%; Score 23.6; DB 9; Length 375;  
Best Local Similarity 74.4%; Pred. No. 1.4e+02;  
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
Qy 2 GGATACCTACTCCCAACATCATCTTACTGATGCAAC 40  
255 GGATATCTACTTGTGACCATCATCTTACTGATGCAAC 217

RESULT 8  
COL17589 738 bp mRNA linear EST 16-JUN-2004  
LOCUS GR\_EB01H15.r GR\_EB Gossypium raimondii cDNA clone GR\_EB01H15 3',  
DEFINITION mRNA sequence.  
ACCESSION COL17589  
VERSION COL17589.1 GI:48816276  
KEYWORDS EST.  
SOURCE Gossypium raimondii  
ORGANISM Gossypium raimondii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosidae; eutroside II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 738)  
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Meller, C.,  
Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and  
Wing, R. A.  
TITLE Global assembly of Cotton ESTs  
JOURNAL Unpublished (2004)  
COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259

Email: twing@genome.arizona.edu  
Plate: 01 row: H column: 15.  
Location/Qualifiers  
1..738  
/organism="Gossypium raimondii"  
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/dev\_stage="3 to +3 DPA"  
/lab\_host="DH10B"  
/clone\_lib="GR\_EB"  
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:  
EcoRV; Library made by Invitrogen with RNA supplied by  
Wendle lab. Directional cloned into NotI-EV. Colonies  
plated/picked by AGI. More glycerol clones held in -80."

ORIGIN  
Query Match 58.0%; Score 23.2; DB 7; Length 738;  
Best Local Similarity 77.8%; Pred. No. 2.2e+02;  
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 4 ATACCTACTCCCAACATCATCTTACTGATGCA 39  
224 ATACACACTCCATACACGCAAGTACATCATGCA 255

RESULT 9  
CR181951 783 bp DNA linear GSS 06-JUL-2004  
LOCUS Reverse strand read from insert in 5'HPRT insertion targeting and  
DEFINITION chromosome engineering clone MHPN361p21, genomic survey sequence.  
ACCESSION CR181951  
VERSION CR181951.1 GI:49360800  
KEYWORDS GSS; Genome survey sequence; MICR.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 783)  
Adams, D. J., Biggs, P. J., Cox, A. V., Davies, R. M., van der Weyden, L.,  
Jonkers, J., Smith, J., Plumb, R. W., Taylor, R. G., Nishijima, I., Yu, Y.,  
Rogers, J. and Bradley, A.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICR

FEATURES  
source  
1..783  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/clone\_lib="MHPN361p21"  
/clone\_lib="MHPN"

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Query Match 58.0%; Score 23.2; DB 11; Length 783;  
Best Local Similarity 77.8%; Pred. No. 2.2e+02;  
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 4 ATACCTACTCCCAACATCATCTTACTGATGCA 39  
514 ATACCTACTCTAAGCAATGATCATCTTACTGATGCA 549

RESULT 10  
CL109241 1018 bp DNA linear GSS 05-JAN-2004  
LOCUS CL109241/c  
DEFINITION ISB1-51D14 Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-51D14,  
genomic survey sequence.  
ACCESSION CL109241  
VERSION CL109241.1 GI:40602876  
KEYWORDS GSS.

SOURCE Xenopus tropicalis (western clawed frog)  
ORGANISM Xenopus tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Silurana.  
REFERENCE 1 (bases 1 to 1018)  
AUTHORS Krametzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,  
Mardis, E., and Wilson, R.  
TITLE A physical map of the xenopus tropicalis genome  
JOURNAL Unpublished (2003)  
COMMENT Contact: Richard K Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert length: 75000 Std Error: 0.00  
Seq primer: SP6 ATTGATGACACATAG  
Class: BAC ends  
High quality sequence start: 72  
High quality sequence stop: 524.  
Location/Qualifiers  
1..1018  
/organism="Xenopus tropicalis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:8364"  
/clone="ISB1-51D14"  
/note="Vector: pBelobAC11; ISB-1 Xenopus tropicalis BAC  
Library Segment 1"

ORIGIN  
Query Match 58.0%; Score 23.2; DB 10; Length 1018;  
Best Local Similarity 77.8%; Pred. No. 2.3e+02;  
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 5 TACCTACTCCCAACATTCATCTTACTCATGCAC 40  
156 TACATCTCCATACATCATTTTATGAAATAC 121

RESULT 11  
CD495749 1253 bp mRNA linear EST 12-UN-2003  
LOCUS CD495749.1 y1d-s SHGC-CD4  
DEFINITION CD495749.1 GI:31422780  
ACCESSION CD495749  
VERSION CD495749.1 GI:31422780  
KEYWORDS EST.  
SOURCE Gaesterosteus aculeatus (three spined stickleback)  
ORGANISM Gaesterosteus aculeatus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Gaesterosteiformes;  
Gaesterosteidae; Gaesterosteus.  
REFERENCE 1 (bases 1 to 1253)  
AUTHORS Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M.,  
Schmutz, J., and Myers, R.M.  
TITLE Expressed sequence tags from Gaesterosteus aculeatus  
JOURNAL Unpublished (2003)  
COMMENT Contact: Kingsley, DM  
HMMI and Department of Developmental Biology  
Stanford University School of Medicine  
Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA  
Tel: 650 725 5954  
Fax: 650 725 7739  
Email: kingsley@cmsgm.stanford.edu  
Plate: 18  
High quality sequence start: 15  
High quality sequence stop: 667.  
Location/Qualifiers  
1..1253  
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/mol\_type="mRNA"  
/strain="Salinas river, CA"

FEATURES  
source

/db\_xref="taxon:69293"  
/clone="CD418-D05"  
/sex="mixed male and female"  
/tissue\_type="heads and internal organs combined"  
/dev\_stage="adult"  
/clone\_id="SHGC-CD4"  
/note="Vector: lambda ZAP Express/pBK-CMV, Site 1: EcoRI  
(5' adaptor); Site 2: XhoI (3' linker primer); The mixed  
organ cDNA library was generated using the ZAP-cDNA method  
by Stratagene. First strand cDNA synthesis was primed with  
a 50 bp linker primer containing an oligo dT sequence  
preceded by a synthetic XhoI site. 5 prime adaptors were  
used inserting an EcoRI cohesive end. The finished cDNAs  
were inserted in to the ZAP express vector  
unidirectionally in the sense orientation with respect to  
the lacZ promoter of pBK-CMV. An amplified library was  
prepared from approximately 3 million primary clones in  
the lambda ZAP Express vector. In vivo excision was then  
used to generate individual pBK-CMV phagemid clones for  
EST sequencing."

ORIGIN  
Query Match 58.0%; Score 23.2; DB 6; Length 1253;  
Best Local Similarity 77.8%; Pred. No. 2.4e+02;  
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 5 TACCTACTCCCAACATTCATCTTACTCATGCAC 40  
1047 TACCTCTTCCCAACATTCATCTTACATCCAC 1082

RESULT 12  
AZ883408 405 bp DNA linear GSS 05-MAR-2001  
LOCUS RPCI-23-18912.TV RPCI-23  
DEFINITION RPCI-23-18912.TV RPCI-23 musculus genomic clone RPCI-23-18912,  
ACCESSION AZ883408  
VERSION AZ883408  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 405)  
AUTHORS Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shutsman, S.,  
Akintel, B., Levins, M., McGinn, S., Tsengaye, G., Geer, K., Krol, M., de  
Jong, P., and Fraser, C.M.  
TITLE Mouse BAC End Sequences from Library RPCI-23  
JOURNAL Unpublished (1999)  
COMMENT Other GSSs: RPCI-23-18912.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC  
library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org). Clones may be purchased from BACPAC  
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end  
page: [http://www.tigr.org/cdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html)  
Seq primer: SP6  
Class: BAC ends.  
Location/Qualifiers  
1..405  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-18912"

FEATURES  
source

/sex="Female"  
/lab host="DH10B"  
/clone\_lib="RPC1-23"  
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1:  
EcORI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methylase. Site  
selected DNA was cloned into the pBAC3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 57.5%; Score 23; DB 9; Length 405;  
Best Local Similarity 74.4%; Pred. No. 2.4e+02;  
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCA 39  
182 AGGTACCAAAATCCCAACATGCTTCTTACTCATGCA 144

RESULT 13

LOCUS C03037346 662 bp mRNA linear EST 22-OCT-2004  
DEFINITION C03037346 full-length enriched swine cDNA library, adult testis Sus  
C03037346 scrofa cDNA clone TES01G080111 5', mRNA sequence.  
C03037346 C03037346.1 GI:54561241  
EST. scrofa (pig)  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 662)  
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,  
Okumura,N., Hamasima,N. and Awata,T.  
PEDE (Pig EST Data Explorer): construction of a database for ESTs  
derived from porcine full-length cDNA libraries  
Nucleic Acids Res. 32 (1), D484-D488 (2004)  
14681463

JOURNAL Contact: Hirohide Uenishi  
PUBMED Animal Genome Laboratory, Genome Research Department  
COMMENT National Institute of Agrobiological Sciences  
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
Tel: +81-29-838-8627  
Fax: +81-29-838-8627  
Email: huenishi@affrc.go.jp  
EST project with full-length enriched cDNA libraries carried out in  
Animal Genome Research Program (Japan) by National Institute of  
Agrobiological Sciences and STRAF-Institute  
Single pass sequencing of clones derived from oligo-capped cDNA  
library  
Vector sequences were eliminated by RepeatMasker version 2002/07/13  
and crossmatch version 0.990319  
Low quality bases were trimmed based on the quality values.

FEATURES

source 1..662  
Location/Qualifiers  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="TES01G080111"  
/tissue\_type="testis"  
/dev\_stage="adult"  
/clone\_lib="full-length enriched swine cDNA library, adult  
testis"

ORIGIN

Query Match 57.5%; Score 23; DB 7; Length 662;  
Best Local Similarity 74.4%; Pred. No. 2.6e+02;  
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCA 39

Db 611 AGGAACCTGACTCCCAACAGCTAGTACTATATCA 649

RESULT 14

LOCUS C0305837 790 bp mRNA linear EST 22-OCT-2004  
DEFINITION C0305837 full-length enriched swine cDNA library, adult testis Sus  
scrofa cDNA clone TES01E060090 5', mRNA sequence.  
C0305837 C0305837.1 GI:54559732  
EST. scrofa (pig)  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 790)  
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,  
Okumura,N., Hamasima,N. and Awata,T.  
PEDE (Pig EST Data Explorer): construction of a database for ESTs  
derived from porcine full-length cDNA libraries  
Nucleic Acids Res. 32 (1), D484-D488 (2004)  
14681463

JOURNAL Contact: Hirohide Uenishi  
PUBMED Animal Genome Laboratory, Genome Research Department  
COMMENT National Institute of Agrobiological Sciences  
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
Tel: +81-29-838-8627  
Fax: +81-29-838-8627  
Email: huenishi@affrc.go.jp  
EST project with full-length enriched cDNA libraries carried out in  
Animal Genome Research Program (Japan) by National Institute of  
Agrobiological Sciences and STRAF-Institute  
Single pass sequencing of clones derived from oligo-capped cDNA  
library  
Vector sequences were eliminated by RepeatMasker version 2002/07/13  
and crossmatch version 0.990319  
Low quality bases were trimmed based on the quality values.

FEATURES

source 1..790  
Location/Qualifiers  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="TES01E060090"  
/tissue\_type="testis"  
/dev\_stage="adult"  
/clone\_lib="full-length enriched swine cDNA library, adult  
testis"

ORIGIN

Query Match 57.5%; Score 23; DB 7; Length 790;  
Best Local Similarity 74.4%; Pred. No. 2.7e+02;  
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 609 AGGAACCTGACTCCCAACAGCTAGTACTATATCA 647

RESULT 15

LOCUS BG506830/c 798 bp mRNA linear EST 27-MAR-2001  
DEFINITION BG506830 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4071154 5',  
mRNA sequence.  
BG506830 BG506830.1 GI:13468347  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.

REFERENCE 1 (bases 1 to 798)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Straubeberg, Ph.D.  
 Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: HLC916 row: e column: 11

FEATURES  
 High quality sequence, stop: 2.  
 Location/Qualifiers  
 1..798

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4071154"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_id="NIH\_MGC\_77"  
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:  
 SfiI (ggcgccgcgcgc); Site 2: SfiI (ggccattatggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGAGCGCGGCACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.9  
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

# ORIGIN

Query Match 57.5%; Score 23; DB 2; Length 798;  
 Best Local Similarity 83.9%; Pred. No. 2.7e+02;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 10 ACTCCCAACATCATCTTACTCATGCAAC 40  
 |||||  
 DB 222 ACTCCCAACAGCCTTCTTACTCATGCAAC 192

Search completed: March 6, 2006, 01:57:49  
 Job time: 188.843 secs

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Best Local Similarity 100.0%; Pred. No. 6e-07;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATCTACTCCCAACATCATCTTACTCATGCAAC 40  
Db 1239 AGGATCTACTCCCAACATCATCTTACTCATGCAAC 1278

## RESULT 2

US-08-880-499-2  
Sequence 2, Application US/08880499  
Patent No. 6037523

GENERAL INFORMATION:

APPLICANT: Albertson, Marc C.

APPLICANT: Fox, Tim W.

APPLICANT: Carl, Garnat W.

APPLICANT: Huffman, Gary A.

APPLICANT: Kendall, Timmy L.

TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION

TITLE OF INVENTION: AND METHOD OF USING SAME

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.

STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.

STREET: Box 1000

CITY: Johnston

STATE: Iowa

COUNTRY: USA

ZIP: 50131

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,499

FILING DATE: CONCURRENTLY HERewith

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Sweeney, Patricia A.

REGISTRATION NUMBER: 32,733

REFERENCE/DOCKET NUMBER: 0578

TELECOMMUNICATION INFORMATION:

TELEPHONE: (515) 248-4800

TELEFAX: (515) 248-4844

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1394 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-880-499-2

Query Match 100.0%; Score 40; DB 3; Length 1394;

Best Local Similarity 100.0%; Pred. No. 6e-07;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATCTACTCCCAACATCATCTTACTCATGCAAC 40  
Db 1239 AGGATCTACTCCCAACATCATCTTACTCATGCAAC 1278

## RESULT 3

US-09-949-002-7790/c

Sequence 7790, Application US/09949002

Patent No. 6900016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000790

CURRENT APPLICATION NUMBER: US/09/949,002  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/231,401  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 10823  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7790

LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-002-7790

Query Match 51.5%; Score 20.6; DB 3; Length 601;

Best Local Similarity 74.3%; Pred. No. 51;

Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ATACCTACTCCCAACATCATCTTACTCATGCA 38  
Db 496 ATAAACACACATCATCATCATCTTCTCATGCA 462

## RESULT 4

US-09-949-002-7791/c

Sequence 7791, Application US/09949002

Patent No. 6900016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000790

CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/231,401

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7791

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-002-7791

Query Match 51.5%; Score 20.6; DB 3; Length 601;

Best Local Similarity 74.3%; Pred. No. 51;

Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ATACCTACTCCCAACATCATCTTACTCATGCA 38  
Db 379 ATAAACACACATCATCATCATCTTCTCATGCA 345

## RESULT 5

US-09-248-796A-5546

Sequence 5546, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 5546

LENGTH: 1071

TYPE: DNA

ORGANISM: Candida albicans

US-09-248-796A-5546

Query Match 51.5%; Score 20.6; DB 3; Length 1071;  
Best Local Similarity 74.3%; Pred. No. 57;  
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 4 ATACCTACTCCCAACATCATCTACTATGCA 38  
DB 224 ATCCCACTCTGACCAACATCTCACTTACTTATTC 258

RESULT 6  
US-09-949-002-782/c  
Sequence 782, Application US/09949002  
Patent No. 6500016

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
FILE REFERENCE: C1000790  
CURRENT APPLICATION NUMBER: US/09/949,002  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/231,401  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 10823  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 782  
LENGTH: 14882  
TYPE: DNA  
ORGANISM: Human

Query Match 51.5%; Score 20.6; DB 3; Length 14882;  
Best Local Similarity 74.3%; Pred. No. 99;  
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 4 ATACCTACTCCCAACATCATCTACTATGCA 38  
DB 8503 ATAAAACACCAATCATCATCTCTCATGCA 8469

RESULT 7  
US-09-949-016-14995/c  
Sequence 14995, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 14995  
LENGTH: 42075  
TYPE: DNA  
ORGANISM: Human

Query Match 51.5%; Score 20.6; DB 3; Length 42075;  
Best Local Similarity 85.2%; Pred. No. 1,28+02;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 4 ATACCTACTCCCAACATCATCTCTTA 30  
DB 31591 ATTCTTACCCACCAACATCTCATCTTA 31565

RESULT 8  
US-09-949-016-65770/c  
Sequence 65770, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 65770  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human

US-09-949-016-65770

Query Match 51.0%; Score 20.4; DB 3; Length 601;  
Best Local Similarity 71.1%; Pred. No. 61;  
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 2 GGATCTACTCTCCCAACATCATCTCTACTATGCA 39  
DB 414 GGATCTCTGGCTGACCAATCTCTCTGCTGAGCA 377

RESULT 9  
US-09-774-528-184  
Sequence 184, Application US/09774528  
Patent No. 6743619

GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Goodrich, Ryle  
APPLICANT: Liu, Chenghua  
APPLICANT: Abundi, Vinod  
APPLICANT: Ren, Feiyang  
APPLICANT: Zhang, Jie  
APPLICANT: Zhao, Qing A.  
APPLICANT: Yang, Yonghong  
APPLICANT: Xue, Aidong J.  
APPLICANT: Wehrman, Tom  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 802  
CURRENT APPLICATION NUMBER: US/09/774,528  
CURRENT FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 441  
SOFTWARE: PC\_FL\_genes Version 2.0  
SEQ ID NO: 184  
LENGTH: 973  
TYPE: DNA  
ORGANISM: Homo sapiens

Query Match 51.0%; Score 20.4; DB 3; Length 973;  
Best Local Similarity 71.1%; Pred. No. 68;

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RESULT 10
US-10-120-988--184
: Sequence 184, Application US/10120988
: Patent No. 6919193
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Goodrich, Ryje
: APPLICANT: Liu, Chenghua
: APPLICANT: Ren, Feiyun
: APPLICANT: Wang, Dunitz
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: No. 6919193el Nucleic Acids and
: TITLE OF INVENTION: Polypeptides
: FILE REFERENCE: 802CON
: CURRENT APPLICATION NUMBER: US/10/120,988
: CURRENT FILING DATE: 2002-04-11
: PRIOR APPLICATION NUMBER: 09/774,528
: PRIOR FILING DATE: 2001-01-30
: NUMBER OF SEQ ID NOS: 441
: SOFTWARE: pc_Fl_genes Version 2.0
: SEQ ID NO 184
: LENGTH: 973
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (231)..(749)
: US-10-120-988--184

```

Query Match	51.0%	Score 20.4	DB 3	Length 973
Best Local Similarity	71.1%	Pred. No. 68		
Matches 27	Conservative 0	Mismatches 11	Indels 0	Gaps 0
Qy	2	GGATACCTACTCCCAACATCATCATCTTACTATCATCAA	39	
Db	626	GGAAATCAACTCCAAAGAAACCCCTCGAAACCATCAA	663	

RESULT 11  
 US-08-945-056-4  
 Sequence 4, Application US/08945056  
 Patent No. 6077994  
 GENERAL INFORMATION:  
 APPLICANT: Coulpland, George M.  
 APPLICANT: Puterill, Joanna J.  
 TITLE OF INVENTION: Genetic control of flowering  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon & Vandervhe PC  
 STREET: 8th Floor, 1100 No. 6077994th Glebe Road  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: United States of America  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/945.056  
 FILING DATE: 20-OCT-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB95/02561  
 FILING DATE: 01-NOV-1995  
 PRIOR APPLICATION DATA:

```

1  APPLICATION NUMBER:  GB 9422083
2  FILING DATE:  02-NOV-1994
3  ATTORNEY/AGENT INFORMATION:
4  NAME:  MB Mary J Wilson
5  REGISTRATION NUMBER:  32,955
6  REFERENCE/DOCKET NUMBER:  620-17
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE:  (703) 816-4900
9  INFORMATION FOR SEQ ID NO:  4:
10  SEQUENCE CHARACTERISTICS:
11  LENGTH:  4201 base pairs
12  TYPE:  nucleic acid
13  STRANDEDNESS:  single
14  TOPOLOGY:  linear
15  MOLECULE TYPE:  DNA (genomic)
16  ORIGINAL SOURCE:
17  ORGANISM:  Arabidopsis thaliana
18  STRAIN:  Landsberg erecta
19  POSITION IN GENOME:
20  MAP POSITION:  chromosome 5
21
22  US-08-945-056-4

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Query Match	51.0%	Score 20.4	DB 3	Length 4201
Best Local Similarity	80.0%	Pred. No. 92		
Matches	24	Conservative	0	Mismatches 6; Indels 0; Gaps 0;
QY	3	GATACCTACTGCCAAACATCATCTACT	32	
DB	2631	GATACCAAGCTCCACACATCATCAACT	2660	

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RESULT 12
US-09-949-016-13668/c
; Sequence 13668, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13668
; LENGTH: 51770
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ..(51770)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13668

```

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Query March 51.0% Score 20.4; DB 3; Length 51770;
Best Local Similarity 71.1% Pred. No. 1.6e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0

Qy 2 GGATPACTTACCTCCCAACATCCATCTTACTCATGCCAA 39
    ||||| | | | | | | | | | | | | | | | |
Db 9851 GGATTCTTGCGCTCAGCAATCTCTCTGCTCAGGCCAA 9814

RESULT 13
US-09-949-016-17420
; Sequence 17420, Application US/09949016
; Patent No. 6812339

```

```

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF.
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 17420
LENGTH: 84571
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(84571)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17420

Query Match
Best Local Similarity 51.0%; Score 20.4; DB 3; Length 84571;
Best Local Similarity 71.1%; Pred. No. 1.7e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 GGATACCTACTCCCAACATCCATCTTACTCATGCAA 39
DB 24559 GGAATCACTCCAAAAGAACCTTCAAAACATGCAA 24596

RESULT 14
US-09-949-016-11824/C
Sequence 11824, Application US/09949016
Patent No. 6812319
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 11824
LENGTH: 126200
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(126200)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11824

Query Match
Best Local Similarity 51.0%; Score 20.4; DB 3; Length 126200;
Best Local Similarity 71.1%; Pred. No. 1.9e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 GGATACCTACTCCCAACATCCATCTTACTCATGCAA 39
DB 53133 GGAATCACTCCAAAAGAACCTTCAAAATCATGCAA 53096

RESULT 15
US-09-949-016-13193/C
Sequence 13193, Application US/09949016
Patent No. 6812319
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 13193
LENGTH: 126200
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(126200)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13193

Query Match
Best Local Similarity 51.0%; Score 20.4; DB 3; Length 126200;
Best Local Similarity 71.1%; Pred. No. 1.9e+02;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 GGATACCTACTCCCAACATCCATCTTACTCATGCAA 39
DB 53133 GGAATCACTCCAAAAGAACCTTCAAAATCATGCAA 53096

Search completed: March 5, 2006, 22:36:28
Job time: 11.1834 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 23:29:11, Search time 57.5163 seconds  
(without alignments)  
5750.985 Million cell updates/sec

Title: US-10-713-381-2\_COPY\_1239\_1278

Perfect score: 40  
Sequence: 1 aggatcctactcccaaacatccttactcgcac 40

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications NA Main:  
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2: /cgn2\_6/ptodata/1/pubpna/us08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/us09\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/us09\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/us10\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/us10\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/us10\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/us10\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/us10\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/us10\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	40	US-10-713-381-6	Sequence 6, Appl1
2	40	100.0	50	US-10-713-381-5	Sequence 5, Appl1
3	40	100.0	158	US-10-713-381-3	Sequence 3, Appl1
4	40	100.0	255	US-10-713-381-9	Sequence 9, Appl1
5	40	100.0	1394	US-10-713-381-1	Sequence 1, Appl1
6	40	100.0	1394	US-10-713-381-2	Sequence 2, Appl1
7	24	60.0	85779	US-10-713-381-6880	Sequence 6880, Ap
8	23.2	58.0	706	US-10-424-599-31006	Sequence 31006, A
9	23	57.5	636	US-09-925-065A-670302	Sequence 670302,
10	22.6	56.5	294	US-10-425-115-143168	Sequence 143168,
11	22.4	56.0	315	US-10-424-599-83179	Sequence 83179, A
12	22.4	56.0	226215	US-10-087-192-1948	Sequence 1948, Ap
13	22.4	55.5	611	US-09-925-065A-591011	Sequence 591011,
14	22.2	55.5	611	US-09-925-065A-591012	Sequence 591012,
15	22.2	55.5	611	US-09-925-065A-591013	Sequence 591013,
16	22.2	55.5	613	US-09-925-065A-253727	Sequence 253727,
17	22	55.0	628	US-09-925-065A-888321	Sequence 888321,
18	21.6	54.0	598	US-09-925-065A-393440	Sequence 393440,
19	21.6	54.0	4110	US-10-473-126-342	Sequence 342, App
20	21.6	54.0	6309	US-10-311-455-277	Sequence 277, App
21	21.4	53.5	560	US-09-925-065A-281837	Sequence 281837,
22	21.4	53.5	560	US-09-925-065A-281838	Sequence 281838,
23	21.4	53.5	620	US-09-925-065A-189248	Sequence 189248,

24	21.4	53.5	653	US-09-925-065A-63167	Sequence 63167, A
25	21.4	53.5	1341	US-09-938-842A-1555	Sequence 1555, Ap
26	21.4	53.5	1341	US-09-938-842A-1555	Sequence 1555, Ap
27	21.4	53.5	6681	US-10-311-455-128	Sequence 128, App
28	21.4	53.5	6681	US-10-240-452-4	Sequence 4, Appl1
29	21.4	53.5	8168	US-10-311-455-901	Sequence 901, Appl1
30	21.4	53.5	8168	US-10-240-454-23	Sequence 23, Appl1
31	21.4	53.5	24401	US-11-097-143-2335	Sequence 2335, Ap
32	21.4	53.5	3673778	US-10-312-841-1	Sequence 1, Appl1
33	21.4	53.5	3673778	US-10-312-841-2	Sequence 2, Appl1
34	21	52.5	293	US-10-424-599-24043	Sequence 24043, A
35	21	52.5	617	US-09-925-065A-285326	Sequence 285327,
36	21	52.5	617	US-09-925-065A-285327	Sequence 285328,
37	21	52.5	617	US-09-925-065A-285328	Sequence 285329,
38	21	52.5	653	US-09-925-065A-597247	Sequence 597247,
39	21	52.5	931	US-10-424-599-20320	Sequence 20320, A
40	21	52.5	2000	US-10-260-238-2594	Sequence 2594, Ap
41	21	52.5	2792	US-10-041-018-361	Sequence 361, App
42	21	52.5	3117	US-10-041-018-362	Sequence 362, App
43	21	52.5	5507	US-10-473-126-198	Sequence 198, App
44	21	52.5	5507	US-10-473-126-344	Sequence 344, App
45	21	52.5	8404	US-10-311-455-1568	Sequence 1568, Ap

## ALIGNMENTS

RESULT 1  
US-10-713-381-6  
Publication US/10713381  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUPFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 5788  
CURRENT APPLICATION NUMBER: US/10/713.381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-6  
Query Match 100.0%; Score 40; DB 8; Length 40;  
Best Local Similarity 100.0%; Pred. No. 4e-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cv 1 AGGATCCTACTCCCAACATCATCTTACTGATGCAC 40  
Db 1 AGGATCCTACTCCCAACATCATCTTACTGATGCAC 40  
RESULT 2  
US-10-713-381-5  
Publication US/10713381  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUPFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 5788

FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-5

Query Match 100.0%; Score 40; DB 8; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.1e-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAC 40  
DB 11 AGGATACCTACTCCCAACATCCATCTTACTCATGCAC 50

RESULT 3  
US-10-713-381-3  
Sequence 3, Application US/10/713,381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 158  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-3

Query Match 100.0%; Score 40; DB 8; Length 158;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAC 40  
DB 86 AGGATACCTACTCCCAACATCCATCTTACTCATGCAC 125

RESULT 4  
US-10-713-381-9  
Sequence 9, Application US/10/713,381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23

NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 255  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-9

Query Match 100.0%; Score 40; DB 8; Length 255;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAC 40  
DB 99 AGGATACCTACTCCCAACATCCATCTTACTCATGCAC 138

RESULT 5  
US-10-713-381-1  
Sequence 1, Application US/10/713,381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1394  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-1

Query Match 100.0%; Score 40; DB 8; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 8e-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAC 40  
DB 1239 AGGATACCTACTCCCAACATCCATCTTACTCATGCAC 1278

RESULT 6  
US-10-713-381-2  
Sequence 2, Application US/10/713,381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFFMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 1394  
TYPE: DNA

ORGANISM: Zea mays  
US-10-713-381-2

Query Match 100.0%; Score 40; DB 8; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 86-06;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGAGTACCTACTCCCAACATCCATCTTCTCATGCAAC 40  
1239 AGATACCTACTCCCAACATCCATCTTCTCATGCAAC 1278

RESULT 7  
US-10-719-993-6880/C

Sequence 6880, Application US/10719993  
Publication No. US20040265849A1

GENERAL INFORMATION:

APPLICANT: Cargill, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: CL001496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6880

LENGTH: 85779

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)...(85779)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-10)

US-10-719-993-6880

Query Match 60.0%; Score 24; DB 8; Length 85779;  
Best Local Similarity 84.4%; Pred. No. 47;

Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

4 ATACTACTCCCAACATCCATCTTCTCATGCAAC 35  
16082 AACTACTCCCAACATCCATCTTCTCATGCAAC 16051

RESULT 8  
US-10-424-599-31006

Sequence 31006, Application US/10424599  
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 31006

LENGTH: 706

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_128002C.1

US-10-424-599-31006

Query Match 58.0%; Score 23.2; DB 7; Length 706;  
Best Local Similarity 77.8%; Pred. No. 39;

Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

5 TACTTACTCCCAACATCCATCTTCTCATGCAAC 40  
TACTTACTCCCAACATCCATCTTCTCATGCAAC 40

Db 455 TCCCTTCCCAACCTCATCACTCATCAAC 490

RESULT 9

US-09-925-065A-670302/C

Sequence 670302, Application US/09925065A

Publication No. US20050228172A3

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 670302

LENGTH: 636

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-670302

Query Match 57.5%; Score 23; DB 4; Length 636;  
Best Local Similarity 74.4%; Pred. No. 45;

Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

1 AGGATCTACTCCCAACATCCATCTTCTCATGCAAC 39  
474 AGGAAACGATTAACAACTATCCACCTTCTCAAGCA 436

RESULT 10

US-10-425-115-143168

Sequence 143168, Application US/10425115

Publication No. US20040214727A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 143168

LENGTH: 294

TYPE: DNA

ORGANISM: Zea mays

OTHER INFORMATION: Clone ID: MRT4577\_62049C.1

US-10-425-115-143168

Query Match 56.5%; Score 22.6; DB 8; Length 294;  
Best Local Similarity 86.2%; Pred. No. 36;

Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

4 ATACTACTCCCAACATCCATCTTCTCATGCAAC 32  
226 ATACTACTCCCAACATCCATCTTCTCATGCAAC 254

RESULT 11  
US-10-424-599-83179  
; Sequence 83179, Application US/10424599  
; Publication No. US20040030172A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Zhou Yihua  
; APPLICANT: Kovalic David K  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 83179  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_46127C.1  
US-10-424-599-83179  
Query Match 56.0%; Score 22.4; DB 7; Length 315;  
Best Local Similarity 81.2%; Pred. No. 69;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 4 ATACTCTCCCAACATCCATCTTACTCAT 35  
DB 211 AACGCACTCCTTAACCAATCCTTAATCCT 242  
RESULT 12  
US-10-087-192-1948  
; Sequence 1948, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US/10/087,192  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1948  
; LENGTH: 226215  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-087-192-1948  
Query Match 56.0%; Score 22.4; DB 5; Length 226215;  
Best Local Similarity 72.5%; Pred. No. 2,5e+02;  
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40  
DB 183206 AGAATTCCTGCTTCACCAACAGCATCTTACTCTTTAC 183245  
RESULT 13  
US-09-925-065A-591011/c  
; Sequence 591011, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 591011  
; LENGTH: 611  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-591011  
Query Match 55.5%; Score 22.2; DB 4; Length 611;  
Best Local Similarity 88.9%; Pred. No. 94;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 14 CCAACATCCATCTTACTCATGCAAC 40  
DB 351 CCAACCAACCACTTACTCATGCAAC 325  
RESULT 14  
US-09-925-065A-591012/c  
; Sequence 591012, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 591012  
; LENGTH: 611  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-591012  
Query Match 55.5%; Score 22.2; DB 4; Length 611;  
Best Local Similarity 88.9%; Pred. No. 94;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 14 CCAACATCCATCTTACTCATGCAAC 40  
DB 351 CCAACCAACCACTTACTCATGCAAC 325  
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US-09-925-065A-591013/c  
; Sequence 591013, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 591013  
LENGTH: 611  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-591013

Query Match 55.54; Score 22.2; DB 4; Length 611;  
Best Local Similarity 88.94; Fred. No. 94;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CCAACATCCATCTTACTCATGCAC 40  
DB 351 CCAACCAACCACTTACTCATGCAC 325

Search completed: March 6, 2006, 03:55:19  
Job time : 59.5163 secs

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OM nucleic - nucleic search, using SW model

Run on: March 6, 2006, 01:58:03 ; Search time 41.7555 Seconds  
(without alignments)  
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Perfect score: 40  
Sequence: 1 aggaatacctactcccaaacatcatcttactcatgcaac 40

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Published Applications NA New:  
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2: /cgn2\_6/pdata/2/pubpna/US06\_NEM\_PUB.seq.\*  
3: /cgn2\_6/pdata/2/pubpna/US07\_NEM\_PUB.seq.\*  
4: /cgn2\_6/pdata/2/pubpna/PCT\_NEM\_PUB.seq.\*  
5: /cgn2\_6/pdata/2/pubpna/US09\_NEM\_PUB.seq.\*  
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12: /cgn2\_6/pdata/2/pubpna/US11\_NEM\_PUB.seq.\*  
13: /cgn2\_6/pdata/2/pubpna/US06\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	23	57.5	636	US-09-925-065A-670302	Sequence 670302, A
C 2	22.6	56.5	3242	US-10-750-185-58624	Sequence 58624, A
C 3	22.6	56.5	3242	US-10-750-623-58624	Sequence 58624, A
C 4	22.2	55.5	611	US-09-925-065A-591011	Sequence 591011, A
C 5	22.2	55.5	611	US-09-925-065A-591012	Sequence 591012, A
C 6	22.2	55.5	611	US-09-925-065A-591013	Sequence 591013, A
C 7	22.2	55.5	611	US-09-925-065A-591014	Sequence 591014, A
C 8	22.2	55.5	611	US-09-925-065A-591015	Sequence 591015, A
C 9	21.6	54.0	598	US-09-925-065A-591016	Sequence 591016, A
C 10	21.4	53.5	560	US-09-925-065A-591017	Sequence 591017, A
C 11	21.4	53.5	560	US-09-925-065A-591018	Sequence 591018, A
C 12	21.4	53.5	560	US-09-925-065A-591019	Sequence 591019, A
C 13	21.4	53.5	560	US-09-925-065A-591020	Sequence 591020, A
C 14	21.4	53.5	560	US-09-925-065A-591021	Sequence 591021, A
C 15	21.4	53.5	560	US-09-925-065A-591022	Sequence 591022, A
C 16	21.4	53.5	560	US-09-925-065A-591023	Sequence 591023, A
C 17	21.4	53.5	560	US-09-925-065A-591024	Sequence 591024, A
C 18	21.4	53.5	560	US-09-925-065A-591025	Sequence 591025, A
C 19	21.4	53.5	560	US-09-925-065A-591026	Sequence 591026, A
C 20	21.4	53.5	560	US-09-925-065A-591027	Sequence 591027, A

21	20.8	52.0	1109	8	US-10-750-185-49907	Sequence 49907, A
22	20.8	52.0	1109	8	US-10-750-623-49907	Sequence 49907, A
23	20.8	52.0	1217	8	US-10-750-185-57406	Sequence 57406, A
24	20.8	52.0	1217	8	US-10-750-623-57406	Sequence 57406, A
C 25	20.6	51.5	50	12	US-11-175-859-103341	Sequence 103341, A
C 26	20.6	51.5	569	6	US-09-925-065A-127036	Sequence 127036, A
C 27	20.6	51.5	586	6	US-09-925-065A-610819	Sequence 610819, A
C 28	20.6	51.5	664	6	US-09-925-065A-696032	Sequence 696032, A
C 29	20.6	51.5	664	6	US-09-925-065A-696033	Sequence 696033, A
C 30	20.6	51.0	201	8	US-10-995-961-70646	Sequence 70646, A
C 31	20.4	51.0	413	6	US-09-925-065A-360599	Sequence 360599, A
C 32	20.4	51.0	470	6	US-09-925-065A-951077	Sequence 951077, A
C 33	20.4	51.0	507	6	US-09-925-065A-589111	Sequence 589111, A
C 34	20.4	51.0	507	6	US-09-925-065A-589112	Sequence 589112, A
C 35	20.4	51.0	507	6	US-09-925-065A-589113	Sequence 589113, A
C 36	20.4	51.0	507	6	US-09-925-065A-589114	Sequence 589114, A
C 37	20.4	51.0	519	6	US-09-925-065A-166725	Sequence 166725, A
C 38	20.4	51.0	545	6	US-09-925-065A-241631	Sequence 241631, A
C 39	20.4	51.0	552	6	US-09-925-065A-785033	Sequence 785033, A
40	20.4	51.0	558	6	US-09-925-065A-659195	Sequence 659195, A
41	20.4	51.0	566	6	US-09-925-065A-910942	Sequence 910942, A
42	20.4	51.0	568	6	US-09-925-065A-104305	Sequence 104305, A
43	20.4	51.0	576	6	US-09-925-065A-573343	Sequence 573343, A
C 44	20.4	51.0	583	6	US-09-925-065A-573822	Sequence 573822, A
C 45	20.4	51.0	583	6	US-09-925-065A-573923	Sequence 573923, A

#### ALIGNMENTS

RESULT 1  
US-09-925-065A-670302/c  
Sequence 670302, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 670302  
LENGTH: 636  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-670302  
Query Match 57.5%; Score 23; DB 6; Length 636;  
Best Local Similarity 74.4%; Pred. No. 11;  
Matches 29; Conservative 0; Mismatches 10; Indels 0;  
Gaps 0;  
Cys 1  
AGGAATCCTACTCCCAACATTCATTCATGCA 39  
Db 474 AGGAATCCTACTCCCAACATTCATTCATGCA 436  
US-10-750-185-58624  
Sequence 58624, Application US/10750185  
Publication No. US20050260603A1  
GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM11100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 58624  
LENGTH: 3242  
TYPE: DNA  
ORGANISM: Bovine 19866880685452  
US-10-750-185-58624

Query Match 56.5%; Score 22.6; DB 8; Length 3242;  
Best Local Similarity 75.7%; Pred. No. 23;  
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 ATACCTACTCCCAACATTCATCTTACTCATGCAAC 40  
DB 2052 ATACCACCTACCAACCACTCAAGCTTATTGATGCAAC 2088

RESULT 3  
US-10-750-623-58624  
Sequence 58624, Application US/10750623  
Publication No. US20050287531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM11100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 58624  
LENGTH: 3242  
TYPE: DNA  
ORGANISM: Bovine 19866880685452  
US-10-750-623-58624

Query Match 56.5%; Score 22.6; DB 8; Length 3242;  
Best Local Similarity 75.7%; Pred. No. 23;  
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 ATACCTACTCCCAACATTCATCTTACTCATGCAAC 40  
DB 2052 ATACCACCTACCAACCACTCAAGCTTATTGATGCAAC 2088

RESULT 4  
US-09-925-065A-591011/c  
Sequence 591011, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 591011  
LENGTH: 611  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-591011

Query Match 55.5%; Score 22.2; DB 6; Length 611;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CCAACAATCCATCTTACTCATGCAAC 40  
DB 351 CCAACAACCACTTACTCATGAGC 325

RESULT 5  
US-09-925-065A-591012/c  
Sequence 591012, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 591012  
LENGTH: 611  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-591012

Query Match 55.5%; Score 22.2; DB 6; Length 611;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CCAACAATCCATCTTACTCATGCAAC 40  
DB 351 CCAACAACCACTTACTCATGAGC 325

RESULT 6  
US-09-925-065A-591013/c  
Sequence 591013, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:

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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 591013
LENGTH: 611
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-591013

Query Match
Best Local Similarity 55.5%; Score 22.2; DB 6; Length 611;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CCNAACATCCATCTTACTGATGCAAC 40
DB 351 CCNAACATCCATCTTACTGATGCAAC 325

RESULT 7
US-09-925-065A-253727
Sequence 253727, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 253727
LENGTH: 613
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-253727

Query Match
Best Local Similarity 55.5%; Score 22.2; DB 6; Length 613;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGAATCTACTCCCAACATCTTACTGATGCA 38
DB 292 GGAATCTACTCCCAACATCTTACTGATGCA 328

RESULT 8
US-09-925-065A-888321/c
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Sequence 888321, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 888321
LENGTH: 628
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-888321

Query Match
Best Local Similarity 55.0%; Score 22; DB 6; Length 628;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGAATCTACTCCCAACATCTTACTGATGCA 39
DB 224 GGAATCTACTCCCAACATCTTACTGATGCA 187

RESULT 9
US-09-925-065A-393490/c
Sequence 393490, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 393490
LENGTH: 598
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-393490

Query Match
Best Local Similarity 54.0%; Score 21.6; DB 6; Length 598;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TATCTCTCTCAATCAATCAATCTTACT 32
DB 228 TATCTCTCTCAATCAATCAATCTTACT 201
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RESULT 10  
US-09-925-065A-281837  
; Sequence 281837, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925, 065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243, 096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252, 147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250, 092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261, 766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289, 846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 281837  
; LENGTH: 560  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-281837

Query Match 53.5%; Score 21.4; DB 6; Length 560;  
Best Local Similarity 71.8%; Pred. No. 46;  
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTGACGA 39  
Db 373 AGGAATCACTCCAAAGAACCTCGAACCATGCA 411

RESULT 11  
US-09-925-065A-281838  
; Sequence 281838, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925, 065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243, 096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252, 147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250, 092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261, 766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289, 846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 281838  
; LENGTH: 560  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-281838

Query Match 53.5%; Score 21.4; DB 6; Length 560;  
Best Local Similarity 71.8%; Pred. No. 46;  
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTGACGA 39

Db 373 AGGAATCACTCCAAAGAACCTCGAACCATGCA 411

RESULT 12  
US-09-925-065A-189248/C  
; Sequence 189248, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925, 065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243, 096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252, 147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250, 092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261, 766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289, 846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 189248  
; LENGTH: 620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-189248

Query Match 53.5%; Score 21.4; DB 6; Length 620;  
Best Local Similarity 75.8%; Pred. No. 47;  
Matches 25; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTGAC 33  
Db 175 ATGATACCTACTCCATCTTATGATGATCTC 143

RESULT 13  
US-09-925-065A-63167  
; Sequence 63167, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925, 065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243, 096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252, 147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250, 092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261, 766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289, 846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63167  
; LENGTH: 653  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-63167

Query Match 53.5%; Score 21.4; DB 6; Length 653;  
Best Local Similarity 71.8%; Pred. No. 47;

Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACATCCATCTTACTGATGCA 39  
DB 186 AGGAACCTACACCTGACATGTCACATCTACTGCA 224

Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 ATACCTACTCCCAACATCCATCTTACTGATGCA 40  
DB 387 ATACCTACTCCCAACATCCATCTTACTGATGCA 423

Search completed: March 6, 2006, 10:32:52  
Job time : 42.7555 secs

RESULT 14  
US-11-124-367A-24503  
; Sequence 24503, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof  
; FILE REFERENCE: C1001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; PRIOR FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24503  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-367A-24503

Query Match 52.5%; Score 21; DB 12; Length 201;  
Best Local Similarity 73.0%; Pred. No. 52;  
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 GATACCTACTCCCAACATCCATCTTACTGATGCA 39  
DB 43 GATACCTGTCTCAAAAATATATTAACATTTAA 79

RESULT 15  
US-09-925-065A-285326  
; Sequence 285326, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 285326  
; LENGTH: 617  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-285326

Query Match 52.5%; Score 21; DB 6; Length 617;  
Best Local Similarity 73.0%; Pred. No. 68;

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RESULT 2
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LOCUS      Male tissue-preferred regulatory region and method of using same.
DEFINITION
ACCESSION      BD062176.1 GI:22607781
VERSION      JP 2001520523-A/1.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1394)
Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and
Kendall,T.L.
Male tissue-preferred regulatory region and method of using same
Patent: JP 2001520523-A 1 30-OCT-2001;
PIONEER HI BRED INTERNATIONAL INC
COMMENT
PN JP 2001520523-A/1
PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAAT,GARY A HUFFMAN,
PI TIMMY L KENDALL
PC C12N15/82,C12N15/29,C12N9/24,C12N9/10,C12N9/00 PC
,C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Best Local Similarity 100.0%; Pred. No. 5.6e-40;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CGGTGTCATCTGCATGCGATGCTGTTGTTCAACCGTTGCTGTTGTCATGCTCC 60
DB      1155 CGGTGTCATCTGCATGCGATGCTGTTGTTCAACCGTTGCTGTTGTCATGCTCC 1214
QY      61 AAGCCTTGCTATTCTGAACCAAGAGATACCTACTCCCAACATGCATCTTACTCATG 120
DB      1215 AAGCCTTGCTATTCTGAACCAAGAGATACCTACTCCCAACATGCATCTTACTCATG 1274
QY      121 CAACTTCATGCAAAACGACATATGTTCTCTGAAC 157
DB      1275 CAACTTCATGCAAAACGACATATGTTCTCTGAAC 1311
RESULT 3
BD062177      1394 bp      DNA      linear      PAT 27-AUG-2002
LOCUS      Male tissue-preferred regulatory region and method of using same.
DEFINITION
ACCESSION      BD062177.1 GI:22607782
VERSION      JP 2001520523-A/2.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1394)
Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and
Kendall,T.L.
Male tissue-preferred regulatory region and method of using same
Patent: JP 2001520523-A 2 30-OCT-2001;
PIONEER HI BRED INTERNATIONAL INC
COMMENT
PN JP 2001520523-A/2
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PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAAT,GARY A HUFFMAN,
PI TIMMY L KENDALL
PC C12N15/82,C12N15/29,C12N9/24,C12N9/10,C12N9/00 PC
,C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Best Local Similarity 100.0%; Pred. No. 5.6e-40;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CGGTGTCATCTGCATGCGATGCTGTTGTTCAACCGTTGCTGTTGTCATGCTCC 60
DB      1155 CGGTGTCATCTGCATGCGATGCTGTTGTTCAACCGTTGCTGTTGTCATGCTCC 1214
QY      61 AAGCCTTGCTATTCTGAACCAAGAGATACCTACTCCCAACATGCATCTTACTCATG 120
DB      1215 AAGCCTTGCTATTCTGAACCAAGAGATACCTACTCCCAACATGCATCTTACTCATG 1274
QY      121 CAACTTCATGCAAAACGACATATGTTCTCTGAAC 157
DB      1275 CAACTTCATGCAAAACGACATATGTTCTCTGAAC 1311
RESULT 4
AX224394      1394 bp      DNA      linear      PAT 10-SEP-2001
LOCUS      Sequence 1 from Patent WO0160997.
DEFINITION      AX224394
ACCESSION      AX224394
VERSION      AX224394.1 GI:15554636
KEYWORDS      Zea mays
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
AUTHORS      Male tissue-preferred regulatory region and method of using same
TITLE      Patent: WO 0160997-A 1 23-AUG-2001;
JOURNAL      PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Best Local Similarity 100.0%; Pred. No. 5.6e-40;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CGGTGTCATCTGCATGCGATGCTGTTGTTCAACCGTTGCTGTTGTCATGCTCC 60
DB      1155 CGGTGTCATCTGCATGCGATGCTGTTGTTCAACCGTTGCTGTTGTCATGCTCC 1214
QY      61 AAGCCTTGCTATTCTGAACCAAGAGATACCTACTCCCAACATGCATCTTACTCATG 120
DB      1215 AAGCCTTGCTATTCTGAACCAAGAGATACCTACTCCCAACATGCATCTTACTCATG 1274
QY      121 CAACTTCATGCAAAACGACATATGTTCTCTGAAC 157
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Db 1275 CAACCTTCATGCAAGACGACATATGTTTCCGTAAC 1311

RESULT 5  
AX224395 1394 bp DNA linear PAT 10-SEP-2001  
LOCUS Sequence 2 from Patent WO0160997.  
DEFINITION AX224395  
ACCESSION AX224395  
VERSION AX224395.1 GI:15554637  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE  
1  
AUTHORS Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL Patent: WO 0160997-A 2 23-AUG-2001;  
PIONEER HI-BRED INTERNATIONAL, INC. (US)

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Best Local Similarity 100.0%; Pred. No. 5.6e-40;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTGTCACTCAGATGCGATCTACTGCTGTTTCAACCGTTGCTGTTCCATGCTCC 60  
Db 1155 CGTGTCACTCAGATGCGATCTACTGCTGTTTCAACCGTTGCTGTTCCATGCTCC 1214  
QY 61 AAGCTTGCCATTATTCGAACCAAGAGATACCTACTCCCAACATCCATCTTACTCANG 120  
Db 1215 AAGCTTGCCATTATTCGAACCAAGAGATACCTACTCCCAACATCCATCTTACTCANG 1274  
QY 121 CAACCTTCATGCAAGACGACATATGTTTCCGTAAC 157  
Db 1275 CAACCTTCATGCAAGACGACATATGTTTCCGTAAC 1311

RESULT 6  
AF360356 3343 bp DNA linear PLN 12-MAY-2001  
LOCUS AF360356  
DEFINITION Zea mays male fertility protein (Ms45) gene, complete cds.  
ACCESSION AF360356  
VERSION AF360356.1 GI:14028756  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE  
1  
AUTHORS Fox, T.W., Trimmell, M.R. and Albertsen, M.C.  
TITLE Cloning of Ms45, a gene required for male fertility from Zea mays  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 3343)  
TITLE Fox, T.W., Trimmell, M.R. and Albertsen, M.C.  
JOURNAL Direct Submission  
TITLE Submitted (13-MAR-2001) Trait and Technology Development, Pioneer  
JOURNAL HI-Bred Intl, Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,  
IA 50131-1004, USA

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Best Local Similarity 100.0%; Pred. No. 5.5e-40;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTGTCACTCAGATGCGATCTACTGCTGTTTCAACCGTTGCTGTTCCATGCTCC 60  
Db 1155 CGTGTCACTCAGATGCGATCTACTGCTGTTTCAACCGTTGCTGTTCCATGCTCC 1214  
QY 61 AAGCTTGCCATTATTCGAACCAAGAGATACCTACTCCCAACATCCATCTTACTCANG 120  
Db 1215 AAGCTTGCCATTATTCGAACCAAGAGATACCTACTCCCAACATCCATCTTACTCANG 1274  
QY 121 CAACCTTCATGCAAGACGACATATGTTTCCGTAAC 157  
Db 1275 CAACCTTCATGCAAGACGACATATGTTTCCGTAAC 1311

RESULT 7  
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LOCUS AX224396  
DEFINITION Sequence 3 from Patent WO0160997.  
ACCESSION AX224396  
VERSION AX224396.1 GI:15554638  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE  
1  
AUTHORS Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.  
TITLE Male tissue-preferred regulatory region and method of using same  
JOURNAL Patent: WO 0160997-A 2 23-AUG-2001;  
PIONEER HI-BRED INTERNATIONAL, INC. (US)

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Matches 157; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 CGTGTCACTCAGATGCGATCTACTGCTGTTTCAACCGTTGCTGTTCCATGCTCC 59  
Db 1 CGTGTCACTCAGATGCGATCTACTGCTGTTTCAACCGTTGCTGTTCCATGCTCC 60  
QY 60 CAAGCTTGCCATTATTCGAACCAAGAGATACCTACTCCCAACATCCATCTTACTCAT 119  
Db 61 CAAGCTTGCCATTATTCGAACCAAGAGATACCTACTCCCAACATCCATCTTACTCAT 120

QY 120 GCACTTCATGCAACACGACATATGTTTCTGAC 157  
DB 121 GCACTTCATGCAACACGACATATGTTTCTGAC 158

RESULT 8  
AP008209\_086/c  
WPCOMMENT

Sequence split into 362 fragments LOCUS AP008209 Accession AP008209

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AP008209_003	300001	410000
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AP008209_006	600001	710000
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AP008209_092	9200001	9310000
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AP008209_094	9400001	9510000
AP008209_095	9500001	9610000
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AP008209_097	9700001	9810000
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AP008209_101	10100001	10210000
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AP008209_104	10400001	10510000
AP008209_105	10500001	10610000
AP008209_106	10600001	10710000
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AP008209_109	10900001	11010000
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AP008209_111	11100001	11210000
AP008209_112	11200001	11310000
AP008209_113	11300001	11410000
AP008209_114	11400001	11510000
AP008209_115	11500001	11610000
AP008209_116	11600001	11710000
AP008209_117	11700001	11810000
AP008209_118	11800001	11910000
AP008209_119	11900001	12010000
AP008209_120	12000001	12110000
AP008209_121	12100001	12210000
AP008209_122	12200001	12310000
AP008209_123	12300001	12410000
AP008209_124	12400001	12510000
AP008209_125	12500001	12610000
AP008209_126	12600001	12710000
AP008209_127	12700001	12810000
AP008209_128	12800001	12910000
AP008209_129	12900001	13010000
AP008209_130	13000001	13110000
AP008209_131	13100001	13210000
AP008209_132	13200001	13310000
AP008209_133	13300001	13410000
AP008209_134	13400001	13510000





RESULT 10  
 AX224398 50 bp DNA PAT 10-SEP-2001  
 LOCUS AX224398  
 DEFINITION Sequence 5 from Patent WO0160997.  
 ACCESSION AX224398  
 VERSION AX224398.1 GI:15554640  
 KEYWORDS  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
 1 Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L. Male tissue-preferred regulatory region and method of using same Patent: WO 0160997-A 5 23-AUG-2001;  
 JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)  
 FEATURES  
 source 1..50  
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 /db\_xref="taxon:4577"

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 3.7e-05;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 CTGAACCAAGAGATACCTACTCCCAACATCCATCTTACTCATGCAAC 124  
 Db 1 CTGAACCAAGAGATACCTACTCCCAACATCCATCTTACTCATGCAAC 50

RESULT 11  
 AX224399 40 bp DNA PAT 10-SEP-2001  
 LOCUS AX224399  
 DEFINITION Sequence 6 from Patent WO0160997.  
 ACCESSION AX224399  
 VERSION AX224399.1 GI:15554641  
 KEYWORDS  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
 1 Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L. Male tissue-preferred regulatory region and method of using same Patent: WO 0160997-A 6 23-AUG-2001;  
 JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)  
 FEATURES  
 source 1..40  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:4577"

ORIGIN  
 Query Match 25.5%; Score 40; DB 6; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.066;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 124  
 Db 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40

RESULT 12  
 BX950854 171896 bp DNA linear VRT 03-FEB-2005  
 LOCUS BX950854  
 DEFINITION Zebrafish DNA sequence from clone CH211-125M22, complete sequence.  
 ACCESSION BX950854  
 VERSION BX950854.12 GI:58190604  
 KEYWORDS HTG.

SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 171896)  
 REFERENCE  
 AUTHORS Pelan, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, GB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk; Clone requests: clonerequests@sanger.ac.uk  
 COMMENT On Jan 25, 2005 this sequence version replaced gi:5636832.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
 -----  
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C\_elegans/wormpep/Clone-derived zebrafish pnc subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.  
 Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhifeng Bao and Sean Eddy, submitted), and those beginning 'Dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D\_rerio/fishmask.shtml  
 CH211-125M22 is from a CHORI-211 BAC library  
 VECTOR: pTARBAC2.1.  
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 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="CH211-125M22"  
 /clone\_lib="CHORI-211"

ORIGIN  
 Query Match 22.2%; Score 34.8; DB 5; Length 171896;  
 Best Local Similarity 52.8%; Pred. No. 3.1;  
 Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 15 TGGCATACATGCTGTTGCAACCGTGTGTTGTCATGTCACAGCTTGCTTAT 74  
 Db 158604 TGGGTTTGTCTCATATCTGACCAACGCTGGGTGTTAAACCAACCCGCTTTAAAGT 158545

Qy 75 CTGAACCAAGAGATACCTACTCCCAACATCCATCTTACTCATGCAAC 134  
 Db 158544 AGGTAACTTCATCTTAATAAAGCTTAAATATTTCATTTAAATCTGAAATCTCAGTTAA 158485

Qy 135 ACAGGCAATATGTTTCGTA 156  
 Db 158484 ACTCCACATTTCTCATTTAA 158463

RESULT 13  
AC104134 110127 bp DNA linear PRI 30-APR-2005  
LOCUS Homo sapiens BAC clone RP11-525L16 from 2, complete sequence.  
DEFINITION AC104134  
AC104134  
VERSION AC104134.4 GI:19551199  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 110127)  
Doehner, A., Haekenson, W. and Tomlinson, C.  
The sequence of Homo sapiens BAC clone RP11-525L16  
JOURNAL Unpublished (2001)  
REFERENCE 2 (bases 1 to 110127)  
AUTHORS Waterston, R.H.  
TITLE Direct Submision  
JOURNAL Submitted (04-DEC-2001) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
3 (bases 1 to 110127)  
REFERENCE 3 (bases 1 to 110127)  
AUTHORS Waterston, R.H.  
TITLE Direct Submision  
JOURNAL Submitted (15-FEB-2002) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
4 (bases 1 to 110127)  
REFERENCE 4 (bases 1 to 110127)  
AUTHORS Waterston, R.H.  
TITLE Direct Submision  
JOURNAL Submitted (20-MAR-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
5 (bases 1 to 110127)  
REFERENCE 5 (bases 1 to 110127)  
AUTHORS Wilson, R.K.  
TITLE Direct Submision  
JOURNAL Submitted (30-APR-2005) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On Mar 20, 2002 this sequence version replaced gi:18677630.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Genetic code: WUGSC  
Web site: http://genome.wustl.edu  
Contact: submissions@wustl.edu  
----- Summary Statistics  
Center project name: H\_NH0525L16  
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NOTICE:  
This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.  
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MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. Wes Warren,  
Department of Genetics, Washington University, St. Louis MO. For  
additional information about the map position of this sequence, see  
http://genome.wustl.edu  
-----  
SOURCE INFORMATION:  
The RPC1-11 human BAC library was made from the blood of one male  
donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,  
Tateo, M., Catanesse, J.J. and de Jong, P.J. (1998) An improved  
approach for construction of bacterial artificial chromosome  
libraries. Genomics 51:1-8. The clone may be obtained either from  
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong

and coworkers at http://www.chori.org  
VECTOR: pBACe3.6  
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NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-554H10, 2000 bp overlap;  
the clone sequenced to the right is RP11-450E9, 2000 bp overlap.  
Actual start of this clone is at base position 15196 of  
RP11-554H10.  
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/db\_xref="taxon:9606"  
/chromosome="2"  
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/clone\_1fb="RPC1-11"  
4046..4309  
/note="CpG island (%GC=61.0, o/e=0.83, #CpGs=20)"  
13008..13484  
/note="CpG island (%GC=75.1, o/e=0.69, #CpGs=53)"  
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/gene="FLJ25369"  
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This gene was based on gi(22749356)"  
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/db\_xref="gi:62988943"  
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DAQLDKFRRIPNPKNKLTGYPAPFRPMPTADLCLRGFPSEGEATREDKRT  
ISTCHFTYPASHDLHLAGDPNQVLOASDFCLVDPKQPAEMAKGTLPLGCPCLH  
CHIVYPIIRNKGPLMPYQ"  
44296..44562  
/note="CpG island (%GC=62.5, o/e=0.89, #CpGs=24)"  
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/note="CpG island (%GC=66.5, o/e=0.76, #CpGs=22)"  
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93417..93529,95828..96048,97869..98091,98748..98886,  
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105456..105650))  
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/note="Homo sapiens eukaryotic translation initiation  
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Continued from H\_NH0450E09.1"  
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DIVIVSAVMKVMNAFSGKGGHLEWYGFCEPIASAWLKQKVPILFDPSTYSN  
DDVLEDESDIVKATGATENSIVYGVWYGOLYSSVYISKFPSPALSYNENA  
IIPLEPTIKKPLIHSPKTPVAVGSDERDKCLSNKFSHEKSNALSLIQTPTNGY  
ILPYKRRNRKSTQITVPLNDPYNKINRKKDVLHWMKEIVATLFCITATTF  
IVRLFHHPHQRKESSTOCOTENKSGVSEANSDSWNDIKSGYSRYLITDEPT  
OCLGGGCVVFEAKNKVDCNVAIKRLPRLRELRKRWREYALAKLHSPGIVRY  
FNMLEAPPEKMGEMDEIWLKDESTWPLSPSPMDAPSVKIRMDPFAIKHEIET

## ORIGIN

Query Match 22.0% Score 34.6; DB 8; Length 110127;  
 Best Local Similarity 54.3%; Prod No. 3.6;  
 Matches 70; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

APSPORSFVSIGISICQTSSESQSFLEPSGMDHEDISEVDAAVNLDSCLTDC  
 VEDGTMDGNDSEHSFELCSSEASPYVRSRERTSSIVEDSGCNDASREKRTNRLH  
 IGRHCKMLTAFPTSSKSSSEATLISIPRTTSLTLTNGCNDASREKRTNRLH  
 QMLCKENLADMMNAGKSEIETREERSVCLHPIQIAVEVEHLSKMLADIKSNIF  
 FTMDDVAVGDFGLVTHMGDDEQVLTVPNPAHNGQVGTSLKMLADIKSNIF  
 HKYDIFSLILFELLYPTSTOMERVLTDVPAHNGQVGTSLKMLADIKSNIF  
 SPMEPEAINIENNAVEDLDPKVTYLRQSRNLSISSGTHSGNSNHPLEBSN

QY 3 TGTCTCTCATGACGATCTACTACATGCTTTTCAACCGTTGCTTGTTCATGTCGA 62  
 DB 87633 TGGGATTCACGAGGACGACGCTACCTGCGAACCATCTTTTCTCTCTTCCA 87692  
 QY 63 GCTTGGCTTATCTGTACCAAGAGATACCTCCAAACATCATCTTACTCTATGCA 122  
 DB 87693 TCTTCCCTATCTTACCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCA 87752  
 QY 123 ACTTCCATG 131  
 DB 87753 ACCTCCAG 87761

RESULT 14  
 AC136896 214946 bp DNA linear PRI 21-MAR-2003  
 LOCUS Homo sapiens chromosome 15, clone RP11-86001, complete sequence.  
 DEFINITION AC136896  
 AC136896.6 GI:29135656  
 ACCESSION HTG  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominoidea; Homo.

REFERENCE  
 AUTHORS Birren, B., Nussbaum, C. and Lander, E.  
 TITLE Homo sapiens chromosome 15, clone RP11-86001  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 214946)

Birren, B., Nussbaum, C., Lander, E., Allen, N., Anderson, S.,  
 Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Boulthager, A.,  
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,  
 Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
 Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
 Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,  
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
 Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,  
 Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J.,  
 Matthews, C., McCarthy, M., McElrath, J., Meneses, L., Minova, T.,  
 Mieng, Y., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Nordu, C.,  
 Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
 Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R.,  
 Riese, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnupack, R.,  
 Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,  
 Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K.,  
 Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (09-NOV-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 214946)

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,  
 Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C.,  
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,  
 McElrath, J., Meneses, L., Minova, T., Mieng, Y., Murphy, T., Naylor, J.,  
 Norman, C., Nicol, R., Nordu, C., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
 Racheva, A., Ramsamy, U., Raymond, C., Retta, R., Riese, C., Rogov, P.,  
 Roman, J., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Smith, C.,  
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,  
 Testaye, S., Theodore, J., Topham, K., Travers, M.,  
 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (23-JAN-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 4 (bases 1 to 214946)

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

COMMENT:  
 Submitted (21-MAR-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 21, 2003 this sequence version replaced gi:21877278.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html.  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: MTBR  
 Web site: http://www-seg.wi.mit.edu  
 Contact: sequence\_submission@genome.wi.mit.edu  
 Project information  
 Center project name: L27824  
 Center clone name: 860\_O\_1  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="15"  
 /map="15"  
 /clone="RP11-86001"  
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 /complement(1..362)  
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 /complement(823..1431)  
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 /complement(2841..3295)  
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 /complement(3307..3311)  
 /note="<30 qual SINGL region"  
 3438..3476  
 /note="single clone coverage"

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repeat_region      /rpt_family="L3"
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repeat_region      complement(8633..8713)
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repeat_region      complement(9299..9498)
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repeat_region      10252..10587      /rpt_family="MLT1A0"
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repeat_region      complement(13183..13354)
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repeat_region      15070..15201      /rpt_family="FLAM-C"
repeat_region      complement(16057..18621)
repeat_region      /rpt_family="L1MB3"
repeat_region      complement(18678..19377)
repeat_region      /rpt_family="L1M1"
repeat_region      complement(19375..20142)
repeat_region      /rpt_family="L1MB3"
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repeat_region      complement(30090..30369)
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repeat_region      32586..32654      /rpt_family="(TCTA)n"
repeat_region      32655..33163      /rpt_family="L1M4"
repeat_region      33164..33473      /rpt_family="AluV"
repeat_region      33474..36683

```

```

repeat_region      /rpt_family="L1M4"
repeat_region      36596..36751      /rpt_family="MLT1D"
repeat_region      36941..37015      /rpt_family="MIR"
repeat_region      complement(38001..38449)
repeat_region      /rpt_family="L1MD1"
repeat_region      38453..38855      /rpt_family="MLT1D"

Query Match      21.9% Score 34.4; DB 8; Length 214946;
Best Local Similarity 54.8%; Pred No.4.2; Mismatches 0; Gaps 0;
Matches 68; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY      5 TCATCTCATGCGATCTACTACTGCTTCTCAACGCTTCTGCTTCATGCTCAAGC 64
         |||||
Db      35745 TCATCTCATGCGCGAAGAAATATCTTGACAAATTCAGCTTCCATGATGTAAC 35804
         |||||

QY      65 CTTCCTATTCTGAAACCAAGAGATACCTACTCCCAACATCTCTTATCATGCAAC 124
         |||||
Db      35805 ATCCAACTACTAGAGAAAGAGTAGCTTCTTAAACCAATMAATGTAACCTATGAAA 35864
         |||||

QY      125 TTCC 128
         |||||
Db      35865 ATCC 35868

```

```

RESULT 15
CR847532      141554 bp      DNA      linear      HTG 15-JAN-2005
LOCUS      Danto rerio clone DKEXP-86C9, WORKING DRAFT SEQUENCE, 3 unordered
DEFINITION      pieces.
ACCESSION      CR847532
VERSION      CR847532.4 GI:57863691
KEYWORDS      HTG: HTGS PHASE1; HTGS ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Danto rerio (zebrafish)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
      Cypriniformes; Cyprinidae; Danto.
      1 (bases 1 to 141554)
REFERENCE      Pelan,S
      Direct Submission
      Submitted (14-JAN-2005) Wellcome Trust Sanger Institute, Hinxton,
      Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
      zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
      On Jan 15, 2005 this sequence version replaced gi:56309949.
COMMENT
      ----- Genome Center
      Center: Wellcome Trust Sanger Institute
      Center code: SC
      Web site: http://www.sanger.ac.uk
      Contact: zfish-help@sanger.ac.uk
      ----- Project Information
      Center project name: zkp86C9
      ----- Summary Statistics
      Assembly program: XGAP4; version 4.5
      Chemistry: Dye-terminator; 100% of reads
      Consensus quality: 141058 bases at least Q40
      Consensus quality: 141224 bases at least Q30
      Consensus quality: 141289 bases at least Q20
      Insert size: 141354; sum-of-contigs
      Insert size: 152619; 10.9% error; agarose-ff
      Quality coverage: 8.68x in Q20 bases; sum-of-contigs Quality
      coverage: 8.12x in Q20 bases; agarose-ff

```

\* NOTE: This is a 'working draft' sequence. It currently
 \* consists of 3 contigs. The true order of the pieces
 \* is not known and their order in this sequence record is
 \* arbitrary. Gaps between the contigs are represented as
 \* runs of N, but the exact sizes of the gaps are unknown.
 \* This record will be updated with the finished sequence
 \* as soon as it is available and the accession number will
 \* be preserved.

FEATURES  
source  
1. 10378: contig of 10378 bp in length  
10379 10478: gap of 100 bp  
10479 42327: contig of 31849 bp in length  
42328 42427: gap of 100 bp  
42428 141554: contig of 99127 bp in length.  
Location/Qualifiers  
1. 141554  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="pKEYP-8609"  
1. 10378  
/note="assembly\_fragment:00017"  
misc\_feature  
10479..42327  
/note="assembly\_fragment:00290"  
misc\_feature  
42428..141554  
/note="assembly\_fragment:00621.0"

ORIGIN  
Query Match 21.5%; Score 33.8; DB 14; Length 141554;  
Best Local Similarity 52.5%; Pred. No. 6.6;  
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 12 ACATGCGATCTACATGCTGTGCAACCGTGTCTGTCATGCTCCATGCTCAAGCCTTGCT 71  
DB 90222 ACAGTGACCCCTACATCTGTGTGCTCATGATGATATGTACAGGTACAGAGTTGGGT 90281  
QY 72 ATTCTGACCAAGAGATACCTACTCCAAATCCATCTTACTCATGCAACTTCCATG 131  
DB 90282 AAGTGGGATATGGGATCATGTGCTCTGAAAATGAAATATCATCACAAAGAACTT 90341  
QY 132 CAAACGCGCATATATGTTCC 152  
DB 90342 TCMAAAAAAATTATATGTC 90362

Search completed: March 5, 2006, 21:55:32  
Job time : 690.29 secs

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CC Present sequence represents a Z. mays Ms45 promoter fragment  
XX Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 157; DB 5; Length 255;  
Best Local Similarity 100.0%; Pred. No. 1.4e-42;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGTGATCTCACATGGCATGCTTGTTCACCGTTCGTTGTCATGCTCC 60  
DB 15 CGGTGATCTCACATGGCATGCTTGTTCACCGTTCGTTGTCATGCTCC 74  
QY 61 AAGCCTTGCTTATTTCTGAACCAAGAGATACCTACTCCCAACATTCATCTTACTCATG 120  
DB 75 AAGCCTTGCTTATTTCTGAACCAAGAGATACCTACTCCCAACATTCATCTTACTCATG 134  
QY 121 CAACTTCATGCAAAACGACATATGTTTCTGTAAC 157  
DB 135 CAACTTCATGCAAAACGACATATGTTTCTGTAAC 171  
RESULT 2  
AA07408  
ID AAX07408 standard; DNA; 1394 BP.  
XX AAX07408;  
AC AAX07408;  
XX 08-JUN-1999 (first entry)  
DT 08-JUN-1999 (first entry)  
XX Zea mays Ms45 male tissue-preferred regulatory region.  
DE Zea mays Ms45 male tissue-preferred regulatory region;  
XX plant tissue; differentiated; maize; hybrid seed; fertility; ss.  
KM plant tissue; differentiated; maize; hybrid seed; fertility; ss.  
XX Zea mays.  
OS Zea mays.  
XX WO9859061-A1.  
XX 30-DEC-1998.  
XX 19-JUN-1998; 98MO-US012895.  
XX 23-JUN-1997; 97US-00880499.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX Albertsen WC, Fox TW, Garmaat CW, Huffman GA, Kendall TL;  
XX WPI; 1999-105628/09.  
XX New nucleic acid encoding a Ms45 male tissue-preferred regulatory region  
PT - useful in mediating plant fertility, especially hybrid seed production.  
XX Claim 2; Page 22-23; 39pp; English.  
XX The sequence is that encoding an Ms45 male tissue-preferred regulatory  
CC region. It may be used in the construction of a vector for a method of  
CC producing exogenous genes in a male tissue-preferred manner, which is  
CC useful in restoring or conferring fertility, such as in hybrid seed  
CC production. In conferring fertility, a monocot/dicot plant is transformed  
CC with the exogenous nucleic acid sequence (a male sterility gene, preferably  
CC Ms45), which encodes a product selected from auxins, rolB and dipteria  
CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile  
CC and infertile plants  
XX Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 157; DB 2; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 2.4e-42;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGTGATCTCACATGGCATGCTTGTTCACCGTTCGTTGTCATGCTCC 60  
DB 15 CGGTGATCTCACATGGCATGCTTGTTCACCGTTCGTTGTCATGCTCC 74

DB 1155 CGGTGATCTCACATGGCATGCTTGTTCACCGTTCGTTGTCATGCTCC 1214  
QY 61 AAGCCTTGCTTATTTCTGAACCAAGAGATACCTACTCCCAACATTCATCTTACTCATG 120  
DB 1215 AAGCCTTGCTTATTTCTGAACCAAGAGATACCTACTCCCAACATTCATCTTACTCATG 1274  
QY 121 CAACTTCATGCAAAACGACATATGTTTCTGTAAC 157  
DB 1275 CAACTTCATGCAAAACGACATATGTTTCTGTAAC 1311  
RESULT 3  
AA07409  
ID AAX07409 standard; DNA; 1394 BP.  
XX AAX07409;  
AC AAX07409;  
XX 08-JUN-1999 (first entry)  
DT 08-JUN-1999 (first entry)  
XX Zea mays Ms45 male tissue-preferred regulatory region.  
DE Zea mays Ms45 male tissue-preferred regulatory region;  
XX plant tissue; differentiated; hybrid seed; fertility; ss.  
KM plant tissue; differentiated; hybrid seed; fertility; ss.  
XX Zea mays.  
OS Zea mays.  
XX WO9859061-A1.  
XX 30-DEC-1998.  
XX 19-JUN-1998; 98MO-US012895.  
XX 23-JUN-1997; 97US-00880499.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX Albertsen WC, Fox TW, Garmaat CW, Huffman GA, Kendall TL;  
XX WPI; 1999-105628/09.  
XX New nucleic acid encoding a Ms45 male tissue-preferred regulatory region  
PT - useful in mediating plant fertility, especially hybrid seed production.  
XX Claim 3; Page 23-24; 39pp; English.  
XX The sequence is that encoding an Ms45 male tissue-preferred regulatory  
CC region. It may be used in the construction of a vector for a method of  
CC producing exogenous genes in a male tissue-preferred manner, which is  
CC useful in restoring or conferring fertility, such as in hybrid seed  
CC production. In conferring fertility, a monocot/dicot plant is transformed  
CC with the exogenous nucleic acid sequence (a male sterility gene, preferably  
CC Ms45), which encodes a product selected from auxins, rolB and dipteria  
CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile  
CC and infertile plants  
XX Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 157; DB 2; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 2.4e-42;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGTGATCTCACATGGCATGCTTGTTCACCGTTCGTTGTCATGCTCC 60  
DB 1155 CGGTGATCTCACATGGCATGCTTGTTCACCGTTCGTTGTCATGCTCC 1214  
QY 61 AAGCCTTGCTTATTTCTGAACCAAGAGATACCTACTCCCAACATTCATCTTACTCATG 120  
DB 1215 AAGCCTTGCTTATTTCTGAACCAAGAGATACCTACTCCCAACATTCATCTTACTCATG 1274  
QY 121 CAACTTCATGCAAAACGACATATGTTTCTGTAAC 157  
DB 1275 CAACTTCATGCAAAACGACATATGTTTCTGTAAC 1311





PT A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the Ms45 gene useful for  
PT mediating fertility in a male plant.  
PS Claim 5, Page 47, 50pp; English.  
XX  
XX The invention provides a male tissue-preferred regulatory region (I)  
XX comprising nucleotide sequences essential for initiating transcription of  
XX the Ms45 gene. A method of mediating male fertility in a plant is  
XX provided that involves introducing an expression vector comprising a  
XX promoter operably linked to (i) into a plant where the exogenous gene  
XX impacts male fertility of the plant and (ii) controls expression of the  
XX exogenous gene. A method of producing hybrid seeds is also provided. The  
XX present sequence represents a DNA fragment -72 to -111 bases upstream of  
XX the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region  
XX nucleotide sequence  
SQ Sequence 50 BP; 18 A; 17 C; 5 G; 10 T; 0 U; 0 Other;  
Query Match 31.8%; Score 50; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 75 CTGAACCAAGAGATCTACTCTCCCAACCAATCCCTTCTACTGCAAC 124  
DB 1 CTGAACCAAGAGATCTACTCTCCCAACCAATCCCTTCTACTGCAAC 50  
RESULT 9  
AAH76337  
ID AAH76337 standard; DNA; 40 BP.  
XX  
XX AAH76337;  
AC  
XX  
XX 29-OCT-2001 (first entry)  
DT  
XX  
XX Z. mays Ms45 male tissue-preferred regulatory region fragment.  
DE  
XX  
XX Ms45; male tissue; regulatory region; transcription; male fertility;  
KM hybrid seed; ds.  
XX  
XX  
OS Zea mays.  
XX  
XX WO200160997-A2.  
PN  
XX  
XX 23-AUG-2001.  
PD  
XX  
XX 13-FEB-2001; 2001WO-US004527.  
PF  
XX  
XX 15-FEB-2000; 2000US-00504487.  
PR  
XX  
XX (PION-) PIONEER HI-BRED INT INC.  
PA  
XX  
XX Albrechtsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;  
PI WPI; 2001-514772/56.  
DR  
XX  
XX A male tissue-preferred regulatory region comprising nucleotide sequences  
PT essential for initiating transcription of the Ms45 gene useful for  
PT mediating fertility in a male plant.  
PS Claim 14; Page 32, 50pp; English.  
XX  
XX The invention provides a male tissue-preferred regulatory region (I)  
XX comprising nucleotide sequences essential for initiating transcription of  
XX the Ms45 gene. A method of mediating male fertility in a plant is  
XX provided that involves introducing an expression vector comprising a  
XX promoter operably linked to (i) into a plant where the exogenous gene  
XX impacts male fertility of the plant and (ii) controls expression of the  
XX exogenous gene. A method of producing hybrid seeds is also provided. The  
XX present sequence represents a DNA fragment upstream of the TATA box of a  
XX Z. mays Ms45 male-tissue preferred regulatory region nucleotide sequence

SQ Sequence 40 BP; 14 A; 14 C; 3 G; 9 T; 0 U; 0 Other;  
Query Match 25.5%; Score 40; DB 5; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 85 AGGATCTACTCTCCCAACCAATCCCTTACTGCAAC 124  
DB 1 AGGATCTACTCTCCCAACCAATCCCTTACTGCAAC 40  
RESULT 10  
ADKS2131  
ID ADKS2131 standard; cDNA; 3267 BP.  
XX  
XX  
XX ADKS2131;  
AC  
XX  
XX 20-MAY-2004 (first entry)  
DT  
XX  
XX Mouse atopic-dermatitis/psoriasis-associated EST #4.  
DE  
XX  
XX Mouse; 88; EST; atopic dermatitis; psoriasis; dermatological;  
KM anti-inflammatory; antipsoriatic; rash; expressed sequence tag.  
XX  
XX  
XX Mus musculus.  
OS  
XX  
XX WO2004016785-A1.  
PN  
XX  
XX 26-FEB-2004.  
PD  
XX  
XX 06-AUG-2003; 2003WO-JP009999.  
PF  
XX  
XX 06-AUG-2002; 2002JP-00229319.  
PR  
XX  
XX 14-MAY-2003; 2003JP-00136544.  
PA  
XX  
XX (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
XX  
XX  
XX Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;  
PI Mitenshi K.  
PI WPI; 2004-214514/20.  
DR  
XX  
XX Detecting atopic dermatitis or psoriasis comprises assaying levels of  
PT expression of an indicator gene at a rash site and non-rash site of a  
PT person with atopic dermatitis or psoriasis.  
XX  
XX  
XX Claim 20; SEQ ID NO 164; 484bp; Japanese.  
PS  
XX  
XX The invention relates to detecting atopic dermatitis or psoriasis  
CC comprising assaying the levels of expression of an indicator gene at a  
CC rash site and non-rash site of a person with atopic dermatitis or  
CC psoriasis, comparing these levels with those of a healthy person, and  
CC determining that if the levels of indicators are higher or lower, then  
CC this indicates the disease. Also included are a reagent for detecting  
CC atopic dermatitis or psoriasis, a kit for screening for treatments, a  
CC transgenic non human vertebrate animal models for the diseases, an agent  
CC for inducing the diseases in mice and a DNA chip for assaying for the  
CC indicator genes. The method is used for treatment, detection and animal  
CC models for research of atopic dermatitis and psoriasis. The present  
CC sequence is a Mouse atopic-dermatitis/psoriasis-associated EST  
XX (expressed sequence tag).  
XX  
XX  
SQ Sequence 3267 BP; 1029 A; 658 C; 590 G; 990 T; 0 U; 0 Other;  
Query Match 20.6%; Score 32.4; DB 12; Length 3267;  
Best Local Similarity 54.1%; Pred. No. 2.5; Indels 0; Gaps 0;  
Matches 66; Conservative 0; Mismatches 56;  
QY 27 TGGCTTGCAACCGTGTGCTTGTTCATGTCGCAAGCCTTCTTTCACACGAG 86  
DB 2774 TGGCTTGCAACCGTGTGCTTGTTCATGTCGCAAGCCTTCTTTCACACGAG 2833

QY 87 GATACCTACTCCGAAACATCTCTTACTCATGCAACTCTTCATGCAACGACATAT 146  
DB 2834 GTTCTAGATTCCTCAAGAACGCTTTTGCACTACGTCAACACTACTAACCTGTAAAT 2893  
QY 147 GT 148  
DB 2894 GT 2895

RESULT 11  
ACA48402/c  
ID ACA48402 standard; DNA; 2352 BP.  
ACA48402;  
19-JUN-2003 (first entry)  
DE Prokaryotic essential gene #30059.  
KW Antisense; ds; prokaryotic essential gene; cell proliferation;  
XX drug design; gene.  
OS Streptococcus mutans.  
XX MO20027183-A2.  
XX 03-OCT-2002.  
XX 21-MAR-2002; 2002MO-US009107.  
XX 21-MAR-2001; 2001US-00815342.  
XX 06-SEP-2001; 2001US-00948993.  
XX 25-OCT-2001; 2001US-0342923P.  
XX 08-FEB-2002; 2002US-00072851.  
XX 06-MAR-2002; 2002US-0362699P.  
XX (ELITR-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zyskind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;  
XX P-PSDB; AB044532.  
XX WPI: 2003-029926/02.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
XX for homologous nucleic acids required for cellular proliferation to  
XX isolate candidate molecules for rational drug discovery programs.  
XX Claim 14; SEQ ID NO 36272; 1766bp; English.

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
CC prokaryotic essential genes. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC XX

Sequence 2352 BP; 762 A; 401 C; 500 G; 689 T; 0 U; 0 Other;

Query Match 20.1%; Score 31.6; DB 8; Length 2352;  
Best Local Similarity 58.5%; Pred. No. 4.2;  
Matches 55; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 62 AGCTTGCTTATTCGAAACGACAGATCTACTCTCCCAACATCATCTTACTATGC 121  
DB 234 ATCTGACGTGTGCCCAACGACCAAGGACATCTCTTAAATACTGTGCTACATCTGC 175  
QY 122 AACTTCATGCAACACGACATATGTTCTCTGA 155  
DB 174 AATTTCAGCAAAAGAACGTTCAATTTTCTCTGA 141

RESULT 12  
ABN80329/c  
ID ABN80329 standard; DNA; 15734 BP.  
XX ABN80329;  
XX 15-JUL-2002 (first entry)  
DE Human chemically modified disease associated gene SEQ ID NO 346.  
XX Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;  
XX heart disease; epilepsy; histone deacetylation; muscular dystrophy;  
XX dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;  
XX antidiabetic; cytostatic; anticonvulsant; ds.  
XX Homo sapiens.  
XX Synthetic.  
XX MO200200927-A2.  
XX 03-JAN-2002.  
XX 02-JUL-2001; 2001MO-EP007536.  
XX 30-JUN-2000; 2000DE-01032529.  
XX 01-SEP-2000; 2000DE-01043826.  
XX (EPIC-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI: 2002-130908/17.  
XX Novel nucleic acid useful for diagnosis and therapy of diseases  
XX associated with development genes such as diabetes, comprises a sequence  
XX of a segment of chemically pretreated DNA of genes associated with  
XX development.  
XX Claim 1; SEQ ID NO 346; 27bp; English.

CC The invention relates to a nucleic acid (I) comprising a sequence at  
CC least 18 bases in length of a segment of chemically pretreated DNA (II)  
CC of genes associated with development selected from 87 genes listed in the  
CC sequences (ABN79984-ABN80333) or their complements. The invention is  
CC useful for the diagnosis or therapy of diseases associated with  
CC development genes, in particular disease related to homeobox containing  
CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes  
CC associated with congenital heart disease, epilepsy, diseases related to

CC histone deacetylation, Curarino syndrome, diseases related with the  
CC development of the brain and limb girdle muscular dystrophy and dwarfism.  
CC Oligomers specific to each of the genes are useful for detecting the  
CC methylation state of all CpG dinucleotides within the 350 sequences or  
CC (II) and their complementary sequences, (III) and/or their complements for  
CC the amplification of the 350 sequences, (II) and/or their complements and  
CC as oligomer probes for detecting the cytosine methylation state and/or  
CC single nucleotide polymorphisms (SNPs). Note: The sequence data for this  
CC patent did not form part of the printed specification but is based on  
CC sequence information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 15734 BP; 3630 A; 744 C; 4234 G; 7126 T; 0 U; 0 Other;  
  
Query Match 20.0%; Score 31.4; DB 6; Length 15734;  
Best Local Similarity 59.6%; Pred. No. 9;  
Matches 53; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
  
QY 52 CCATGTCACAGCTTGCCTTATCTGAAACCAAGAGTACTCTCCAAACATCTC 111  
DB 8802 CTTCTCTTCTCCCTTATGCAATCTTAAACATCAAAACCTTAAATAAACAACCAAC 8743  
QY 112 TTAAGTATGACACTTCCATGCAACAGC 140  
DB 8742 TACCTAACCACTCTTCAATTAACACC 8714  
  
RESULT 13  
AAF22279  
ID AAF22279 standard; DNA; 64415 BP.  
AC AAF22279;  
DT 20-MAR-2001 (first entry)  
DE BAC containing repeats from centromeres 1-4 #2.  
KM Centromere; mitochromosome; vector; ds.  
XX  
XX Arabidopsis thaliana.  
OS  
XX  
XX Arabidopsis thaliana.  
PN WO20005325-A2.  
XX  
PD 21-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-US007392.  
XX  
XX 18-MAR-1999; 99US-0125219P.  
PR 01-APR-1999; 99US-0127409P.  
PR 18-MAY-1999; 99US-0134770P.  
PR 13-SEP-1999; 99US-0153584P.  
PR 17-SEP-1999; 99US-0154603P.  
PR 16-DEC-1999; 99US-0172493P.  
XX  
XX (UYCH-) UNIT CHICAGO.  
PA  
XX  
XX Preuss D, Copenhagen G, Keith K,  
PI  
XX  
XX WPI, 2000-587529/55.  
DR  
XX  
XX Recombinant DNA construct comprising a plant centromere, useful for  
PT producing stably inherited mitochromes which can serve as vectors for the  
PT construction of transgenic plant and animal cells.  
XX  
XX Claim 102; Page 321-335; 1449p; English.  
XX  
XX The present invention relates to a recombinant DNA construct of a plant  
CC (Arabidopsis thaliana) centromere. The constructs are useful for  
CC producing stably inherited mitochromes which can serve as vectors for the  
CC construction of transgenic plant and animal cells expressing selected  
CC proteins such as hormones, enzymes, interleukins, clotting factors,  
CC cytokines, antibodies, and growth factors  
XX  
XX Sequence 64415 BP; 18698 A; 13554 C; 13083 G; 18980 T; 0 U; 100 Other;

Query Match 19.5%; Score 30.6; DB 3; Length 64415;  
Best Local Similarity 58.1%; Pred. No. 26;  
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
  
QY 65 CTGGCTTATCTGAACCAAGAGTATCTACCTCCAAACATCTTATCATGCAAC 124  
DB 7117 CTGGCTTATCTGAACCAAGAGTATCTACCTCCAAACATCTTATCATGCAAC 7116  
QY 125 TTTCATGGAACAGCAGCATATGTTCTCGAAC 157  
DB 7177 TTAAATCCCAACCTTAATCTAATCTTAAAC 7209  
  
RESULT 14  
ADA02717  
ID ADA02717 standard; DNA; 79467 BP.  
AC ADA02717;  
DT 06-NOV-2003 (first entry)  
DE Mouse Nfatcl carcinoma associated gene, SEQ ID NO:1235.  
XX  
XX Mouse Nfatcl carcinoma associated gene, SEQ ID NO:1235.  
XX  
XX Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;  
KM prostate; lymphoma; leukemia; cytostatic; gene therapy; drug screening;  
KM gene; ds.  
XX  
XX Mus sp.  
OS  
XX  
XX WO2003057146-A2.  
XX  
XX 17-JUL-2003.  
XX  
XX 26-DEC-2002; 2002WO-US041414.  
XX  
XX 26-DEC-2001; 2001US-00035832.  
XX  
XX (SAGR-) SAGRES DISCOVERY.  
PA  
XX  
XX Morris DW;  
PI  
XX  
XX WPI, 2003-587068/55.  
DR  
XX  
XX New recombinant nucleic acid encoding carcinoma associated protein,  
PT useful for preparing compositions for treating carcinomas.  
XX  
XX Claim 1; SEQ ID NO 1235; 245p; English.  
XX  
XX The invention relates to recombinant carcinoma associated (CA) nucleic  
CC acid sequences from mouse and human (ADA01482-ADA03094), and to  
CC recombinant carcinoma associated proteins (CAP) encoded by them. The  
CC invention also encompasses expression vectors and host cells comprising a  
CC CA nucleic acid, a polypeptide (especially an antibody) that specifically  
CC binds to the protein, and a biochip comprising CA nucleic acid or  
CC fragments thereof. The sequences of the invention were identified using  
CC oncogenic retroviruses, which insert into the genome of the host organism  
CC at random. Many of these do not carry transduced host oncogenes or  
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a  
CC direct consequence of the effects of proviral integration into host  
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose  
CC leukemias or a propensity to carcinoma by determination of the sequence  
CC of a CA gene, or by determination of CA gene expression in particular  
CC tissues. CA nucleic acids, proteins and antibodies are also useful as  
CC therapeutic agents and in screening and evaluating drug candidates. The  
CC present sequence represents a specifically claimed murine CA nucleic acid  
CC sequence of the invention. Note: The complete sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic form directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 79467 BP; 18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;

Query Match 19.5%; Score 30.6; DB 9; Length 79467;  
Best Local Similarity 56.4%; Pred. No. 28;  
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Search completed: March 5, 2006, 18:11:35  
Job time : 107.48 secs

QY 51 TCCATGCTCAAGCCTTGCTTATTCGAAACCAAGAGATCTACTCCCAACATCCAT 110  
DB 53779 TCCACTTAAGTCTGCTTCTCTGGAACAAGCTGAGTCTTAGTCACACACACACA 53838  
QY 111 CTTACTCATGCACTTCATGCAACAACGACATATGTTTC 151  
DB 53839 CACACACACACACACACACACACACACAGCTTGCGCTC 53879

RESULT 15  
ADB72455  
ID ADB72455 standard; DNA; 79467 BP.  
XX  
AC ADB72455;

XX 04-DEC-2003 (first entry)

XX Mouse Nfatc1 gene.

XX mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;  
XX cancer; neoplasm; adenocarcinoma; sarcoma; gene.

XX Mus sp.

XX MO2003008583-A2.

XX 30-JAN-2003.

XX 26-DEC-2001; 2001MO-US051291.

XX 02-MAR-2001; 2001US-00798586.

XX 23-OCT-2001; 2001US-0004113.

XX 08-NOV-2001; 2001US-00052482.

XX 30-NOV-2001; 2001US-0097722.

XX 20-DEC-2001; 2001US-00034650.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW, Engelhard EK;

XX WPI; 2003-239337/23.

XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,  
XX cancers, neoplasm, adenocarcinoma, or sarcomas.

XX Claim 1; SEQ ID NO 283; 2304bp; English.

XX The invention relates to a novel recombinant nucleic acid comprising a  
XX nucleotide sequence selected from any of the 660 sequences fully defined  
XX in the specification. A polynucleotide of the invention has cytotatic  
XX activity, and may have a use in gene therapy, or in a vaccine. The  
XX recombinant nucleic acids and polypeptides are useful for treating  
XX carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and  
XX sarcomas. The present sequence represents a mouse gene of the invention.

XX Sequence 79467 BP; 18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;

Query Match 19.5%; Score 30.6; DB 10; Length 79467;

Best Local Similarity 56.4%; Pred. No. 28;  
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 51 TCCATGCTCAAGCCTTGCTTATTCGAAACCAAGAGATCTACTCCCAACATCCAT 110  
DB 53779 TCCACTTAAGTCTGCTTCTCTGGAACAAGCTGAGTCTTAGTCACACACACACA 53838

QY 111 CTTACTCATGCACTTCATGCAACAACGACATATGTTTC 151  
DB 53839 CACACACACACACACACACACACACACAGCTTGCGCTC 53879



|||||  
Db 421 CGGTGATCTGCATGCGATGCTGCTGTTCAACCGTTGCTGTTTCATGCTCC 362  
|||  
Qy 61 AAGCCTTGCTTATTGGAACCAAGAGATACCTACTGCCAAACATCCATCTTACTCATG 120  
|||  
Db 361 AAGCCTTGCTTATTGGAACCAAGAGATACCTACTGCCAAACATCCATCTTACTCATG 302  
|||  
Qy 121 CAACCTTCATGCAACACGACCATATGTTTCTGTAAC 157  
|||  
Db 301 CAACCTTCATGCAACACGACCATATGTTTCTGTAAC 265  
|||  
RESULT 2  
CG224225 915 bp DNA linear GSS 22-AUG-2003  
LOCUS OGIAG08TV ZM 0.7\_1.5\_KB Zea mays genomic clone ZMMBMA0716B15,  
DEFINITION genomic survey sequence.  
ACCESSION CG224225  
VERSION CG224225  
KEYWORDS GS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 915)  
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGIAG08TV  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@cigr.org  
Seq primer: TF  
Classes: methylation filtered.  
Location/Qualifiers  
1..915  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZMMBMA0716B15"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

FEATURES  
source

ORIGIN

Query Match 100.0%; Score 157; DB 10; Length 915;  
Best Local Similarity 100.0%; Pred. No. 2.4e-39;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
|||  
Qy 1 CGGTGATCTGCATGCGATGCTGCTGTTCAACCGTTGCTGTTTCATGCTCC 60  
|||  
Db 534 CGGTGATCTGCATGCGATGCTGCTGTTCAACCGTTGCTGTTTCATGCTCC 593  
|||  
Qy 61 AAGCCTTGCTTATTGGAACCAAGAGATACCTACTGCCAAACATCCATCTTACTCATG 120  
|||  
Db 594 AAGCCTTGCTTATTGGAACCAAGAGATACCTACTGCCAAACATCCATCTTACTCATG 653  
|||  
Qy 121 CAACCTTCATGCAACACGACCATATGTTTCTGTAAC 157  
|||  
Db 654 CAACCTTCATGCAACACGACCATATGTTTCTGTAAC 690  
|||  
RESULT 3  
CC656933 963 bp DNA linear GSS 19-JUN-2003  
LOCUS CGMDQ20TV ZM 0.7\_1.5\_KB Zea mays genomic clone ZMMBMA0554D15,  
DEFINITION

genomic survey sequence.  
ACCESSION CC656933  
VERSION CC656933.1 GI:32060225  
KEYWORDS GS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 963)  
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: CGMDQ20TV  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@cigr.org  
Seq primer: TF  
Classes: methylation filtered.  
Location/Qualifiers  
1..963  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZMMBMA0554D15"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

FEATURES  
source

ORIGIN

Query Match 100.0%; Score 157; DB 9; Length 963;  
Best Local Similarity 100.0%; Pred. No. 2.4e-39;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
|||  
Qy 1 CGGTGATCTGCATGCGATGCTGCTGTTCAACCGTTGCTGTTTCATGCTCC 60  
|||  
Db 752 CGGTGATCTGCATGCGATGCTGCTGTTCAACCGTTGCTGTTTCATGCTCC 811  
|||  
Qy 61 AAGCCTTGCTTATTGGAACCAAGAGATACCTACTGCCAAACATCCATCTTACTCATG 120  
|||  
Db 812 AAGCCTTGCTTATTGGAACCAAGAGATACCTACTGCCAAACATCCATCTTACTCATG 871  
|||  
Qy 121 CAACCTTCATGCAACACGACCATATGTTTCTGTAAC 157  
|||  
Db 872 CAACCTTCATGCAACACGACCATATGTTTCTGTAAC 908  
|||  
RESULT 4  
CW324514 702 bp DNA linear GSS 31-OCT-2004  
LOCUS CW324514  
DEFINITION 104 819 11477203 148 35910 078 Sorghum methylation filtered library  
(LibID: 104) Sorghum bicolor genomic clone 11477203, genomic survey  
sequence.  
ACCESSION CW324514  
VERSION CW324514.1 GI:55040702  
KEYWORDS GS.  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 702)  
Jones, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
McMenamy, J., Smith, M., Rohlfing, T., Fries, J., Bradford, K.,  
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Deddelon, J.A. and  
Martensen, R.A.

**TITLE** Sorghum genome sequencing by methylation filtration  
**JOURNAL** J. Biol. Chem. 275 (2000) 15660-15665  
**PUBMED** 15660154  
**COMMENT** Contact: Bedell JA  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Orlon Genomics, LLC  
 Tel: 314 615 6975  
 Fax: 314 615 5975  
 Email: jbedell@origenomics.com  
 Plate: 819 Row: C Column: 19  
 Seq primer: SMF Forward  
 Class: methylation filtered  
 High quality sequence stop: 702.  
**FEATURES**  
 source  
 1..702  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /cultivar="ATx623"  
 /db\_xref="taxon:4558"  
 /clone="11477203"  
 /clone\_lib="Sorghum methylation filtered library (Libid: 104)"  
 /note="Organ: leaf; Vector: pBSCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."  
**ORIGIN**  
 Query Match 40.1%; Score 63; DB 10; Length 702;  
 Best Local Similarity 91.0%; Pred. No. 3.9e-09;  
 Matches 66; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 64 CTTGCGCTATTCTGAACCAAGAGATACCTACTCCCAACATCTTACTCATGCA 123  
 |||||  
 Db 53 CCTGCGCTATTCTGAACCAAGAGACACTTACTCCCAACATCTTACTCATGCA 112  
 |||||  
 QY 124 CTTGCGCTAA 134  
 |||||  
 Db 113 CTTGCGCTAA 123  
**RESULT 5**  
**LOCUS** CMA45575 296 bp DNA linear GSS 02-NOV-2004  
**DEFINITION** fdbb001f170m16k6 Sorghum methylation filtered library (Libid: 104)  
 Sorghum bicolor genomic clone fdbb001f170m16, genomic survey  
 sequence.  
**ACCESSION** CMA45575  
**VERSION** CMA45575.1 GI:55193536  
**KEYWORDS** GSS.  
**SOURCE** Sorghum bicolor (sorghum)  
**ORGANISM** Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 296)  
 Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
 Jones, J., Plick, E., Rohlfing, T., Fries, J., Bradford, K.,  
 McManamy, J., Smith, M., Holman, H., Roe, B.A., Wiley, G., Korfi, I. F.,  
 Rablinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and  
 Martienssen, R.A.  
 Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)  
**TITLE** Sorghum genome sequencing by methylation filtration  
**JOURNAL** PLOS Biol. 3 (1), e13 (2005)  
**PUBMED** 15660154  
**COMMENT** Contact: Bedell JA  
 Orlon Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6975  
 Fax: 314 615 5975  
 Email: jbedell@origenomics.com  
 Plate: fdbb001f170 Row: m Column: 16

**TITLE** Seq primer: k Reverse  
 Class: methylation filtered  
 High quality sequence stop: 296.  
**FEATURES**  
 source  
 1..296  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /cultivar="ATx623"  
 /db\_xref="taxon:4558"  
 /clone="fbb001f170m16"  
 /clone\_lib="Sorghum methylation filtered library (Libid: 104)"  
 /note="Organ: leaf; Vector: pBSCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."  
**ORIGIN**  
 Query Match 29.9%; Score 47; DB 10; Length 296;  
 Best Local Similarity 85.3%; Pred. No. 0.00042;  
 Matches 64; Conservative 0; Mismatches 10; Indels 1; Gaps 1;  
 QY 64 CTTGCGCTATTCTGAACCAAGAGATACCTACTCCCAACAT-CCATCTTACTCATGCA 122  
 |||||  
 Db 221 CCTGCGCTATTCTGAACCAAGAGACACTTACTCCCAACATCCCATGTTACCATGCA 280  
 |||||  
 QY 123 ACTTCCATGCAACA 137  
 |||||  
 Db 281 ACTTCCATGCAACA 295  
**RESULT 6**  
**LOCUS** CE588104/c 636 bp DNA linear GSS 28-SEP-2003  
**DEFINITION** tigr-gss-dog-17000366359543 Dog library Canis familiaris genomic,  
 genomic survey sequence.  
**ACCESSION** CE588104  
**VERSION** CE588104.1 GI:36904885  
**KEYWORDS** GSS.  
**SOURCE** Canis familiaris (dog)  
**ORGANISM** Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Placentalia; Canidae;  
 Canis.  
 1 (bases 1 to 636)  
 Kirkness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,  
 Busch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
**TITLE** The dog genome: survey sequencing and comparative analysis  
**JOURNAL** Science 301 (5641), 1898-1903 (2003)  
**PUBMED** 14512627  
**COMMENT** Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.  
**FEATURES**  
 source  
 1..636  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"  
**ORIGIN**  
 Query Match 24.1%; Score 37.8; DB 10; Length 636;

Best Local Similarity 58.4%; Pred. No. 0.48;  
Matches 66; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 45 TCTTGTTCATCGTCCAGCGCTTGCCATCTGACCAAGAGAGATCCCTACCCAAACA 104  
Db 292 TATTTTTCCTCCATTCAGGATCTCTGTTTGACCCAGGATACCTCATTTTAAAA 233.

QY 105 ATCCATCTTACTGATGCAACTTCATGCAAAACGACATATGTTCTGTAAC 157  
Db 232 ATACATTTTATATAGAAATTTTCAAAACCAAAATTAATGCTGATGTAAC 180

RESULT 7  
CO689495 643 bp mRNA linear EST 26-JUL-2004  
LOCUS DG11-2516  
DEFINITION  
ACCESSION CO689495  
VERSION CO689495.1 GI:50638161  
KEYWORDS  
SOURCE  
ORGANISM  
Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
1 (bases 1 to 643)  
Schlueter, T., Hermanns, J., Weindel, M., Schlueter, D., Kranz, H.,  
Henrich, J., and Loebbert, R.  
Dog arraytag cdna clone collection  
Unpublished (2004)  
Contact: Thomas Schlueter  
LION Bioscience AG  
Walhoferstrasse 98, D-69123 Heidelberg, Germany  
Tel: +49 6221 4038 150  
Fax: +49 6221 4038 290  
Email: Thomas.Schlueter@lionbioscience.com.

FEATURES  
source  
1..643  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/strain="Beagle"  
/db\_xref="taxon:9615"  
/tissue\_type="kidney"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="DG11-kidney"  
/note="Organ: kidney; Vector: Dog pBluescript LION"

ORIGIN  
Query Match 24.1%; Score 37.8; DB 7; Length 643;  
Best Local Similarity 58.4%; Pred. No. 0.49;  
Matches 66; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 45 TCTTGTTCATCGTCCAGCGCTTGCCATCTGACCAAGAGATCCCTACCCAAACA 104  
Db 333 TATTTTTCCTCCATTCAGGATCTCTGTTTGACCCAGGATACCTCATTTTAAAA 274

QY 105 ATCCATCTTACTGATGCAACTTCATGCAAAACGACATATGTTCTGTAAC 157  
Db 273 ATACATTTTATATAGAAATTTTCAAAACCAAAATTAATGCTGATGTAAC 221

RESULT 8  
AG366773 1085 bp DNA linear GSS 21-DEC-2004  
LOCUS AG366773  
DEFINITION  
ACCESSION AG366773  
VERSION AG366773.1 GI:47977978  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus molossinus (Japanese wild mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE  
AUTHORS  
1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwa, K. and Shiroishi, T.  
TITLE  
Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis  
JOURNAL  
PUBMED  
1574823  
Genome Res. 14 (12), 2439-2447 (2004)

REFERENCE  
AUTHORS  
2 (bases 1 to 1085)  
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE  
Direct Submission  
Submitted (17-NOV-2003) Maaahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenho-chou, Tsukuba, Ibaraki, Japan, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
COMMENT  
Clones are derived from the mouse BAC library MSM01. For BAC library availability, please contact Kunihya Abe (abe@tc.riken.jp).  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koydai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@tc.riken.jp  
PRIMERS  
Sequencing : TV  
LIBRARY  
Vector : pBAC3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.  
Location/Qualifiers  
1..1085  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSM01-170B12.TJ"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_lib="MSM01 Mouse Male BAC Library"

ORIGIN  
Query Match 24.1%; Score 37.8; DB 10; Length 1085;  
Best Local Similarity 51.9%; Pred. No. 0.57;  
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 22 CTACATGCTTGTTCACCGTGTGCTTGTTCATGCTCCAGCGCTTGCTATTCGAAC 81  
Db 719 CTCCT 660

QY 82 AAGAGATACCTTACCTCCAAACATCATCTTACTGATGCAAACTTCATGCAAAACGCA 141  
Db 659 ACATTAATTAACCCCCCAANNAAACCAANNAAACCCGCAATTTTANANANATAAA 600

QY 142 CATATGTTCTCTG 154  
Db 599 CAATCTTTTCTG 587

RESULT 9  
CZ727957 874 bp DNA linear GSS 25-JUL-2005  
LOCUS CZ727957  
DEFINITION  
ACCESSION CZ727957  
VERSION CZ727957.1 GI:71136431  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza coarctata (Porteresia coarctata)  
Oryza coarctata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 874)  
AUTHORS Kim, H., Collura, K., Wisotski, M., Byrne, M., Stum, D., Smart, D., Rao, K., Luo, M., Jetly, R., Kudrna, D., Muller, C., Soderlund, C. and Wang, R.  
TITLE OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute  
JOURNAL Unpublished (2005)  
COMMENT Contact: Rod A. Wang  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1255  
Email: rtwing@genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Plate: 0055 row: 1 column: 24  
Seq primer: TAA TAC GAC TCA CTA TAG GG  
Class: BAC ends.  
FEATURES  
source  
1..874  
/organism="Oryza coarctata"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:77588"  
/clone="OC\_Ba0055L24"  
/tissue\_type="leaves"  
/dev\_stage="mature"  
/lab\_host="DH10B"  
/clone\_1lb="OC\_Ba"  
/note="Vector: pUGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

ORIGIN  
Query Match 22.7%; Score 35.6; DB 10; Length 874;  
Best Local Similarity 78.6%; Pred. No. 2.7;  
Matches 55; Conservative 0; Mismatches 14; Indels 1; Gaps 1;  
QY 64 CTTGCGCTATTCGACCAAGAGGATACCTTCCCAACATTCATCTTACGATGAA 123  
DB 778 CTTGCGCTATTCGACCAAGGACG-CACCTACTCTCAAAACATCAGCGGATCATGAGA 836  
QY 124 CTTGCGATGCA 133  
DB 837 CTTGCGATGCA 846

RESULTS 10  
BB505306 700 bp mRNA linear EST 25-OCT-2001  
LOCUS BB505306 RIKEN full-length enriched, 10 days lactation, adult  
DEFINITION female mammary gland Mus musculus cDNA clone D730002G06, mRNA  
sequence.  
ACCESSION BB505306 GI:16442791  
VERSION BB505306  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 700)  
AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanasaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komuro, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
Unpublished (2001)  
On Jul 27, 2000 this sequence version replaced gi:9514268.  
CONTACT Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute.

The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenho-cho, Tsukuba-shi, Ibaraki, 305-8565, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.jp URL: <http://genome.gsc.riken.jp/>  
Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K., Itoh, M., Komuro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Komuro, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001).  
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamakata, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.  
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001).  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
FEATURES  
source  
1..700  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="D730002G06"  
/sex="female"  
/tissue\_type="mammary gland"  
/dev\_stage="10 days lactation, adult"  
/lab\_host="DH10B"  
/clone\_1lb="RIKEN full-length enriched, 10 days lactation, adult female mammary gland"  
/note="Site 1: SalI; Site 2: BamHI. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',  
GAGAGAGAGCGCGCGACACTGCGATTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5',  
GGAAGAGATTCGAGTTATTTATTTATTTATTCCTCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLO-1."

ORIGIN  
Query Match 21.7%; Score 34; DB 2; Length 700;  
Best Local Similarity 54.9%; Pred. No. 8.3;  
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;  
QY 27 TGCCTTGTCACCGTGGTCTTGTTCATGCTCCAGCTTGCTTATTCGAAACCAAG 86  
DB 195 TTTCTTTTTCGCCCTCCCTCTATTTCTTTTACACCTTCACTTTTGGCTTTAGTT 254  
QY 87 GATACCTACCTCCCAACATCATCTTTCACGACCACTTCAGCAACAGCAACATAT 146

Db 255 GTTCTAGATTCCCAAGAACCATTTTGCATGACTCAAGCACTACTAACACCTTGAAAT 314  
Qy 147 GT 148  
Db 315 GT 316

RESULT 11  
LOCUS CM871670/c 734 bp DNA linear GSS 12-FEB-2005  
DEFINITION she2h63-44.g 013.ab1 Whole-genome shotgun library of the elephant shark (aka elephant fish) Callorhynchus milli genomic, genomic survey sequence.  
ACCESSION CM871670  
VERSION CM871670.1 GI:59698305  
KEYWORDS GSS.  
SOURCE Callorhynchus milli (elephantfish)  
ORGANISM Callorhynchus milli

REFERENCE  
AUTHORS Venkatesh, B., Tay, A., Dandona, N., Patil, J. G. and Brenner, S.  
TITLE 1 (bases 1 to 734)  
JOURNAL Holoccephali; Chimaeriformes; Callorhynchidae; Callorhynchus.  
PUBMED Curr. Biol. 15 (3), R82-R83 (2005)  
COMMENT A compact cartilaginous fish model genome  
Contact: Venkatesh B  
Molecular Genetics Lab  
Institute of Molecular and Cell Biology  
61 Biopolis Drive, Singapore 138673  
Tel: 65 6586 9571  
Fax: 65 6779 1117  
Email: mcbyv@imcb.a-star.edu.sg  
Whole-genome shotgun sequences of the elephant shark (aka elephant fish)  
Class: shotgun.  
Location/Qualifiers  
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/organism="Callorhynchus milli"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7866"  
/sex="Male"  
/tissue\_type="Testis"  
/clone\_lib="Whole-genome shotgun library of the elephant shark (aka elephant fish)"

ORIGIN  
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Best Local Similarity 54.4%; Pred. No. 9.8;  
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

LOCUS 1 CGTGTCACTCAGATGGCATACTACATGCTGTTCACCGTGTGTTCCATCGTCC 60  
Db 238 CGTGGCATTTCAATTGCACTCCACGCGATTATGCGATCGCACTGTGTTAATGACCC 179  
Qy 61 AAGCTTGGCTTATTTGGAACCAAGAGATACCTACTCCCAACATCATTACTCATG 120  
Db 178 GAATACACACCAACCAACACCAACACATACACCAACACCACTTTAACAAGA 119  
Qy 121 CAACT 125  
Db 118 AATCT 114

RESULT 12  
LOCUS CL026582 1677 bp DNA linear GSS 31-DEC-2003  
DEFINITION CH216-23G24\_Sp6.1 CH216 Xenopus tropicalis genomic clone  
ACCESSION CL026582  
VERSION CL026582.1 GI:40470443  
KEYWORDS GSS.  
SOURCE Xenopus tropicalis (western clawed frog)  
ORGANISM Xenopus tropicalis

REFERENCE  
AUTHORS Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.  
TITLE A physical map of the xenopus tropicalis genome  
JOURNAL Unpublished (2003)  
COMMENT Contact: Richard K Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert Length: 175000 Std Error: 0.00  
Seq primer: Sp6 ATTTAGTGCACCTATAG  
Class: BAC ends  
High quality sequence start: 125  
High quality sequence stop: 217.  
Location/Qualifiers  
1..1677  
/organism="Xenopus tropicalis"  
/mol\_type="genomic DNA"  
/strain="Nigerian frog"  
/db\_xref="taxon:8364"  
/clone="CH216-23G24"  
/sex="male"  
/cell\_line="Stock 248 F7A2, inbred N7"  
/clone\_lib="CH216"  
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"

ORIGIN  
Query Match 21.4%; Score 33.6; DB 10; Length 1677;  
Best Local Similarity 53.9%; Pred. No. 15;  
Matches 69; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

LOCUS 3 TGTCACTCAGATGGCATACTACATGCTGTTCACCGTGTGTTCCATCGGCCA 62  
Db 769 TGTGCTTCATCAGATGCACTTCTCGATTCCTTTGCTCTTACAGTGTTCATCGGTT 828  
Qy 63 GCCTTCCCTATTCTGAACCAAGAGATACCTACTCCCAACATCATTACTCATGCA 122  
Db 829 TCACTCACTATTCTTCACTGATGATGACCTCTCTCACTTTCTATATTTATTCAGCA 888  
Qy 123 ACTTCAT 130  
Db 889 TCTTCAT 896

RESULT 13  
LOCUS A1744861 440 bp mRNA linear EST 21-JUN-1999  
DEFINITION t16b06.x1 NCI\_CGAP\_OV23 Homo sapiens cDNA clone IMAGE:2218451 3', mRNA sequence.  
ACCESSION A1744861  
VERSION A1744861.1 GI:5113149  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 440)  
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center









Db 940 CACACATTTGTTTGTCCACCAAGAGCTTACATTTCTCCAGACATATCTA 881  
QY 95 CTCACCAACATCATCTTACTCA 118  
Db 880 ATCCCTAGAGATGCTTTTATAT 857

## RESULT 5

US-09-557-884-1/C

; Sequence 1, Application US/09557884

; Patent No. 6506581

; GENERAL INFORMATION:

; APPLICANT: Fleischmann et al.

; TITLE OF INVENTION: The Nucleotide sequence of

; the Haemophilus influenzae Rd Genome, Fragments

; thereof, and Uses Thereof

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 1/2 inch diskette

; OPERATING SYSTEM: MS DOS v6.22

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/557,884

; FILING DATE: 25-Apr-2000

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/476,102

; FILING DATE: JUN-5-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Michelle S. Marks

; REGISTRATION NUMBER: 41,971

; REFERENCE/DOCKET NUMBER: PB186P3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1830121 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

; US-09-557-884-1

; Query Match

; Best Local Similarity 18.6%; Score 29.2; DB 3; Length 1830121;

; Matches 67; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

; QY 12 ACATGGCATCTACATGCTTGTTCACCGTTCCTGTTCCATGTCACAGCTTGCT 71

; Db 677275 ACTTAAATTCAGCTGCTGCTGCTCTATTTGATTTGATTAATGCAAGATAGCT 677216

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; Db 677215 ATGCTGCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 677156

; QY 132 CAAACAGCA 141

; Db 677155 CAACCAACCA 677146

; RESULT 6

US-09-643-990A-1/C

; Sequence 1, Application US/09643990A

Patent No. 6528289  
GENERAL INFORMATION:  
APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith  
J. Craig Venter  
TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville,  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A  
FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426,787  
FILING DATE: 1995-04-21  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB186P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1  
Query Match  
Best Local Similarity 18.6%; Score 29.2; DB 3; Length 1830121;  
Matches 67; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
QY 12 ACATGGCATCTACATGCTTGTTCACCGTTCCTGTTCCATGTCACAGCTTGCT 71  
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QY 72 ATTCTGAACCAAGAGATACCTACTCCCAACATTCATCTTATGCACTTCATG 131  
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QY 132 CAAACAGCA 141  
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## RESULT 7

US-10-158-865-1/C

; Sequence 1, Application US/10158865

; Patent No. 684651

; GENERAL INFORMATION:

; APPLICANT: Fleischmann et al.

; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragm

; Patent No. 684651

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? TITLE OF INVENTION: Thereof, and Uses Thereof
? FILE REFERENCE: PB16P2C1D1
? CURRENT APPLICATION NUMBER: US/10/158,865
? CURRENT FILING DATE: 2002-06-03
? PRIOR APPLICATION NUMBER: US 09/557,884
? PRIOR FILING DATE: 2000-04-25
? PRIOR APPLICATION NUMBER: US 08/476,102
? PRIOR FILING DATE: 1995-06-07
? PRIOR APPLICATION NUMBER: US 08/426,787
? PRIOR FILING DATE: 1995-04-21
? NUMBER OF SEQ ID NOS: 1
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 1
? LENGTH: 1830121
? TYPE: DNA
? ORGANISM: Haemophilus influenzae
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? LOCATION: (4747)..(4747)
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GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14,755  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15502  
; LENGTH: 11022  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15502

Query Match 17.8%; Score 28; DB 3; Length 11022;

Best Local Similarity 63.2%; Pred. No. 27;  
Matches 43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 15 TGGCATACATGCTGTTTCAACCGTTCGCTGTTTCATGTCAGCCTTGCTATT 74  
DB 4432 TGGCTATTTCATGCTGTTTTCAGGTTATGTTAGCATTCATTCAGCCTTGTCAGG 4491

QY 75 CTGAACCA 82  
DB 4492 CTGAATCA 4499

RESULT 11

US-09-949-016-17447  
; Sequence 17447, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17447  
; LENGTH: 41815  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-17447

Query Match 17.8%; Score 28; DB 3; Length 41815;

Best Local Similarity 58.3%; Pred. No. 43;  
Matches 49; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 62 AGCCTTGCTATTCTGAACCAAGAGATACCTACCTCCCAACAATCCATCTTACTCATGC 121  
DB 33058 AGACATGCAATTCACACACATCCGATAGCTGCTCTAGGATCCTGCTCACTCATTC 33117

QY 122 AACTTCATGCAACGACGACATA 145  
DB 33118 ATGTCAATAGAGACATGATGTA 33141

RESULT 12

US-09-949-016-191201/C  
; Sequence 191201, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 191201  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-191201

Query Match 17.7%; Score 27.8; DB 3; Length 601;

Best Local Similarity 58.0%; Pred. No. 11;  
Matches 47; Conservative 1; Mismatches 33; Indels 0; Gaps 0;

QY 57 GTCCAAAGCCTTGCCTTATTCGAACCAAGAGATACCTACCTCCCAACAATCCATCTTACT 116  
DB 322 GTCTGACCTTGATGATCCACACATCGGCGCAACACACACACTCTCTCATTT 263

QY 117 CATGCACTTCCATGCAACA 137  
DB 262 CATGCAATGATGATGGAATA 242

RESULT 13

US-09-949-016-14149/C  
; Sequence 14149, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14149  
; LENGTH: 11490  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14149

Query Match 17.7%; Score 27.8; DB 3; Length 11490;

Best Local Similarity 52.1%; Pred. No. 32;  
Matches 62; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 38 CCGTTGCTCTGTTCCATGTCCTAAGCCTTGGCTTATTCGAAACAGAGATACCTACTC 97  
DB 5642 CAGGGCTCTGCTTCCTCCCTCCCTCCCTGCCCCACCTCACAGAGAAAGCCACGC 5583

QY 98 CCAACATGCATCTTACTGATGCAATTCATGCAACGACGACATATGTTCTGAA 156  
DB 5582 CTTGCAACCTGATGCAATCCACATCCGCTTGATGAGGAGGAGATGTTGCCCAA 5524

RESULT 14  
US-09-949-016-16740  
Sequence 16740, Application US/09949016  
Patent No. 6812338  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMOPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16740  
LENGTH: 14952  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-16740

Query Match 17.7%; Score 27.8; DB 3; Length 14952;  
Best Local Similarity 59.5%; Pred. No. 35;  
Matches 47; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 67 TGCCTATTCTGAACCAAGAGATCTACTCCCAACATCCATCTTACTGACCACTT 126  
DB 70 TGTCAACCGTATCCAAAGATATATTAGTTTAGAGATTCTCTCTCAAGGTAACTA 129

QY 127 CCATGCAACGCGACAT 145  
DB 130 GGTTTACACACACACA 148

RESULT 15  
US-09-937-862B-37  
Sequence 37, Application US/09937862B  
Patent No. 6846621  
GENERAL INFORMATION:  
APPLICANT: Oberste, M. Steven  
APPLICANT: Maher, Kaija  
APPLICANT: Kilpatrick, David R.  
APPLICANT: Pallansch, Mark A.  
TITLE OF INVENTION: TYPING OF HUMAN ENTEROVIRUSES  
FILE REFERENCE: 14114.035302  
CURRENT APPLICATION NUMBER: US/09/937,862B  
PRIOR FILING DATE: 2001-09-28  
PRIOR APPLICATION NUMBER: PCT/US00/07828  
PRIOR FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: 60/127,464  
PRIOR FILING DATE: 1999-03-31  
NUMBER OF SEQ ID NOS: 89  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 37  
LENGTH: 927  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence; No. 6846621e =  
US-09-937-862B-37

Query Match 17.6%; Score 27.6; DB 3; Length 927;  
Best Local Similarity 55.1%; Pred. No. 15;  
Matches 54; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 53 CATGTCACAGCCTTGCTATTCTGAACCAAGAGATCTACTCCCAACATCATCT 112

DB 551 CATGTCACAGCCTTGCTATTCTGAACCAAGAGATCTACTCCCAACATCATCT 610  
QY 113 TACTGATGCACTTCATGCAAGACGACATATGTT 150  
DB 611 CTTTGTGGCACTTACAAAGCGGTACTGACATTTTAT 648

Search completed: March 5, 2006, 22:36:21  
Job time: 48.8947 secs

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GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFEMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1394  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-1

Query Match 100.0%; Score 157; DB 8; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 3.8e-43;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGTGATCTCACATGCGATACATGCTGTTCAACCGTTCGCTGTTGCATGCTCC 60  
Db 1155 CGGTGATCTCACATGCGATACATGCTGTTCAACCGTTCGCTGTTGCATGCTCC 1214  
Qy 61 AAGCCTTGCTTATTTGGAACGAGAGATGCTACTGCCAAACATCCATCTTACTCATG 120  
Db 1215 AAGCCTTGCTTATTTGGAACGAGAGATGCTACTGCCAAACATCCATCTTACTCATG 1274  
Qy 121 CACTTCATGCAACACGACATATGTTCTGTAAC 157  
Db 1275 CACTTCATGCAACACGACATATGTTCTGTAAC 1311

RESULT 3  
US-10-713-381-2  
Sequence 2, Application US/10713381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFEMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 1394  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-2

Query Match 100.0%; Score 157; DB 8; Length 1394;  
Best Local Similarity 100.0%; Pred. No. 3.8e-43;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGTGATCTCACATGCGATACATGCTGTTCAACCGTTCGCTGTTGCATGCTCC 60  
Db 1155 CGGTGATCTCACATGCGATACATGCTGTTCAACCGTTCGCTGTTGCATGCTCC 1214  
Qy 61 AAGCCTTGCTTATTTGGAACGAGAGATGCTACTGCCAAACATCCATCTTACTCATG 120

Db 1215 AAGCCTTGCTTATTTGGAACGAGAGATGCTACTGCCAAACATCCATCTTACTCATG 1274  
Qy 121 CACTTCATGCAACACGACATATGTTCTGTAAC 157  
Db 1275 CACTTCATGCAACACGACATATGTTCTGTAAC 1311

RESULT 4  
US-10-713-381-3  
Sequence 3, Application US/10713381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFEMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 158  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-3

Query Match 93.0%; Score 146; DB 8; Length 158;  
Best Local Similarity 99.4%; Pred. No. 1e-39;  
Matches 157; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGGTGATCTCACATGCGATACATGCTGTTCAACCGTTCGCTGTTGCATGCTCC 59  
Db 1 CGGTGATCTCACATGCGATACATGCTGTTCAACCGTTCGCTGTTGCATGCTCC 60  
Qy 60 CAAGCCTTGCTTATTTGGAACGAGAGATGCTACTGCCAAACATCCATCTTACTCATG 119  
Db 61 CAAGCCTTGCTTATTTGGAACGAGAGATGCTACTGCCAAACATCCATCTTACTCATG 120  
Qy 120 GCACTTCATGCAACACGACATATGTTCTGTAAC 157  
Db 121 GCACTTCATGCAACACGACATATGTTCTGTAAC 158

RESULT 5  
US-10-713-381-5  
Sequence 5, Application US/10713381  
Publication No. US20040221331A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARNAT, CARL W.  
APPLICANT: HUFEMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-5

Query Match 31.8%; Score 50; DB 8; Length 50;  
Best Local Similarity 100.0%; Pred. No. 57e-07;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 75 CTGAACCAAGAGATCTACTCTCCCAACATTCATTTTCATGCAAC 124  
1 CTGAACCAAGAGATCTACTCTCCCAACATTCATTTTCATGCAAC 50

RESULT 6  
US-10-713-381-6  
Sequence 6, Application US/10713381  
Publication No. US2004021311A1  
GENERAL INFORMATION:  
APPLICANT: ALBERTSEN, MARC C.  
APPLICANT: FOX, TIMOTHY W.  
APPLICANT: GARMAN, CARL W.  
APPLICANT: HUPPMAN, GARY  
APPLICANT: KENDALL, TIMMY L.  
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF  
FILE REFERENCE: 578R  
CURRENT APPLICATION NUMBER: US/10/713,381  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 08/880,499  
PRIOR FILING DATE: 1997-06-23  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-713-381-6

Query Match 25.5%; Score 40; DB 8; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 85 AGGATCTACTCTCCCAACATTCATTCATGCAAC 124  
1 AGGATCTACTCTCCCAACATTCATTCATGCAAC 40

RESULT 7  
US-10-674-124A-9081/C  
Sequence 9081, Application US/10674124A  
Publication No. US20040197797A1  
GENERAL INFORMATION:  
APPLICANT: INOKO, Hidetoshi  
APPLICANT: TAMURA, Gen  
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE  
FILE REFERENCE: ORIN-003CIP  
CURRENT APPLICATION NUMBER: US/10/674,124A  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 10/257,511  
PRIOR FILING DATE: 2003-03-07  
PRIOR APPLICATION NUMBER: PCT/JP00/07621  
PRIOR FILING DATE: 2000-10-30  
PRIOR APPLICATION NUMBER: JP2000-112659  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: JP2002-327516  
PRIOR FILING DATE: 2002-09-28  
PRIOR APPLICATION NUMBER: JP2002-383869  
PRIOR FILING DATE: 2002-12-09  
NUMBER OF SEQ ID NOS: 27110  
SEQ ID NO 9081  
LENGTH: 399  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: chr5.fa.07ftr.139538206

FEATURE:  
OTHER INFORMATION: Located on chromosome 5  
FEATURE:  
OTHER INFORMATION: Distance between a terminus base of telomere on  
OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base  
OTHER INFORMATION: sequence : 128437212  
FEATURE:  
OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and  
OTHER INFORMATION: 5'-terminus of this base sequence : 250186  
US-10-674-124A-9081

Query Match 20.5%; Score 32.2; DB 8; Length 399;  
Best Local Similarity 61.2%; Pred. No. 1.67  
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
DB 72 ATTCTGAACCAAGAGATCTACTCTCCCAACATTCATTCATGCAACTTCATG 131  
239 ATTCTGAACCAAGAGATCTACTCTCCCAACATTCATTCATGCAACTTCATG 180  
DB 132 CAACACGACATATGTTCTGTA 156  
179 AAAAAACACACATTTGTGTGTA 155

RESULT 8  
US-10-282-122A-36272/C  
Sequence 36272, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: EITRA 0348  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See file wrapper or PAM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 36272  
LENGTH: 2352  
TYPE: DNA  
ORGANISM: Streptococcus mutans

US-10-282-122A-36272

Query Match 20.1%; Score 31.6; DB 7; Length 2352;  
Best Local Similarity 58.5%; Pred. No. 4.9;  
Matches 55; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 62 AGCTTGCTTATCTGACCAAGAGTACCTGCTCCCAACATCATCTCAATGC 121  
DB 234 ATCTGCTGCTGCTCCCAAGCAAGCAAGCATCTCTGAAATCTGCTCATCTGC 175  
QY 122 AACTTCATGCAACAGCAATATCTTCTCA 155  
DB 174 AATTTCAGCAAAAGACGTTCAATTTTCTCA 141

RESULT 9

US-09-925-065A-871704  
Sequence 871704, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925, 065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243, 096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252, 147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250, 092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261, 766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289, 846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 871704  
LENGTH: 565  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-871704

Query Match 20.0%; Score 31.4; DB 4; Length 565;  
Best Local Similarity 60.2%; Pred. No. 3.4;  
Matches 50; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 4 GTCATCTCACATGCGCATATCATGCTTGTCAACCGTGTCTTGTTCATGCTCAAG 63  
DB 274 GGCCTCTGCTGAGAGAGCCCATGCTTGAAGCCCTTGTCTCGTCTTGAAT 333  
QY 64 CTTGCTTATCTGCAACCAAGAG 86  
DB 334 TCATGATATATTTGACCAAGAG 356

RESULT 10

US-09-925-065A-778732/c  
Sequence 778732, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925, 065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243, 096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252, 147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250, 092

PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261, 766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289, 846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 778732  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-778732

Query Match 19.6%; Score 30.8; DB 4; Length 601;  
Best Local Similarity 52.3%; Pred. No. 5.5;  
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 12 ACATGCTACTACATGCTTGTTCACCGTGTCTGTCTTCATGCTCCAGCTTGGCT 71  
DB 354 ACATGCTACTACATGCTTGTTCATGCTGTGCTATAGATATTTATACCTTGGCT 295  
QY 72 ATTCTGACCAAGAGATACCTACTCCCAACATCATCTTACTCATGCACTTCATG 131  
DB 294 ATTATTAATGATTAATTTTCTATACATACAGTTTCTACCCATATATCTTCTTA 235  
QY 132 CAACACAGCA 141  
DB 234 AACACTGACA 225

RESULT 11

US-10-437-963-1496/c  
Sequence 1496, Application US/10437963  
Publication No. US2004012343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovacic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437, 963  
PRIOR FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 1496  
LENGTH: 1122  
TYPE: DNA  
ORGANISM: Oryza sativa  
FEATURES:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_101357C.1  
US-10-437-963-1496

Query Match 19.6%; Score 30.8; DB 7; Length 1122;  
Best Local Similarity 57.1%; Pred. No. 7;  
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 60 CAAGCTTGCTTATCTGACCAAGAGATACCTACTCCCAACATCATCTTACTCAT 119  
DB 313 CAGGCTCGATATTTGATCCGGGATACATAAATCAACAAAGCATATTTACTTCT 254  
QY 120 GCACTTCCATGCAACAGCAATATGTTTCTGTAAC 157  
DB 253 TCAGATCCAAATCGACCCCTCCATATCTGCTGAAC 216

RESULT 12

US-10-027-632-244811  
Sequence 244811, Application US/10027632

```
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIORITY FILING DATE: 2002-04-30
PRIORITY FILING DATE: 2002-04-30
PRIORITY FILING DATE: 2000-07-12
PRIORITY FILING DATE: 2000-07-12
PRIORITY FILING DATE: 2000-04-20
PRIORITY FILING DATE: 2000-03-29
PRIORITY FILING DATE: 2000-02-24
PRIORITY FILING DATE: 2000-02-24
PRIORITY FILING DATE: 1999-11-23
PRIORITY FILING DATE: 1999-09-28
PRIORITY FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 244811
LENGTH: 559
TYPE: DNA
ORGANISM: Human
US-10-027-632-244811

Query Match      19.5%; Score 30.6; DB 5; Length 559;
Best Local Similarity 51.9%; Pred. No. 6.3;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 24 ACATGCTGTTCACCGTTCCTGTCATGTCGCAACCTTCCTATTCGACCA 83
DB 380 ACATGCTATTCGATCTTTCATTTGCTGCTGAGGTACTTTTCTAGATTC 439
QY 84 GAGGATACCTACTCCCAACATCCATCTTACTGACGACTTCGACCAACGCCCA 143
DB 440 TCTGCTCCCTACTTTAAGATTCATGAGATCTTCAAAATCCATAGACACTGAC 499
QY 144 TATGTTCTCTGAA 156
DB 500 ATTTCTTCCCA 512

RESULT 13
US-10-027-632-244811
Sequence 244811, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIORITY FILING DATE: 2002-04-30
PRIORITY FILING DATE: 2002-04-30
PRIORITY FILING DATE: 2000-07-12
PRIORITY FILING DATE: 2000-04-20
PRIORITY FILING DATE: 2000-03-29
PRIORITY FILING DATE: 2000-03-29
PRIORITY FILING DATE: 2000-02-24
PRIORITY FILING DATE: 2000-02-24
PRIORITY FILING DATE: 1999-11-23
PRIORITY FILING DATE: 1999-09-28
PRIORITY FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
```

```
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 244811
LENGTH: 559
TYPE: DNA
ORGANISM: Human
US-10-027-632-244811

Query Match      19.5%; Score 30.6; DB 6; Length 559;
Best Local Similarity 51.9%; Pred. No. 6.3;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 24 ACATGCTGTTCACCGTTCCTGTCATGTCGCAACCTTCCTATTCGACCA 83
DB 380 ACATGCTATTCGATCTTTCATTTGCTGCTGAGGTACTTTTCTAGATTC 439
QY 84 GAGGATACCTACTCCCAACATCCATCTTACTGACGACTTCGACCAACGCCCA 143
DB 440 TCTGCTCCCTACTTTAAGATTCATGAGATCTTCAAAATCCATAGACACTGAC 499
QY 144 TATGTTCTCTGAA 156
DB 500 ATTTCTTCCCA 512

RESULT 14
US-10-052-482-223
Sequence 223, Application US/10052482
GENERAL INFORMATION:
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71087/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
PRIORITY FILING DATE: 2000-12-22
PRIORITY FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 241
SOFTWARE: PatentIn version 3.1
SEQ ID NO 223
LENGTH: 79467
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (4099)..(4369)
OTHER INFORMATION: "n" at positions 4099 to 4369 can be any base
FEATURE:
NAME/KEY: misc.feature
LOCATION: (5502)..(5521)
OTHER INFORMATION: "n" at positions 5502 to 5521 can be any base
FEATURE:
NAME/KEY: misc.feature
LOCATION: (10089)..(10620)
OTHER INFORMATION: "n" at positions 10089 to 10620 can be any base
FEATURE:
NAME/KEY: misc.feature
LOCATION: (13273)..(13370)
OTHER INFORMATION: "n" at positions 13273 to 13370 can be any base
FEATURE:
NAME/KEY: misc.feature
LOCATION: (20762)..(20781)
OTHER INFORMATION: "n" at positions 20762 to 20781 can be any base
FEATURE:
NAME/KEY: misc.feature
LOCATION: (30751)..(30916)
OTHER INFORMATION: "n" at positions 30751 to 30916 can be any base
FEATURE:
NAME/KEY: misc.feature
LOCATION: (46579)..(46772)
OTHER INFORMATION: "n" at positions 46759 to 46772 can be any base
```

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (77382)..(77401)  
OTHER INFORMATION: "n" at positions 77372 to 77401 can be any base  
US-10-052-482-223

Search completed: March 6, 2006, 03:55:07  
Job time : 227.751 secs

Query Match 19.5%; Score 30.6; DB 7; Length 79467;  
Best Local Similarity 56.4%; Pred. No. 39;  
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 51 TTCATGCTGCAAGCCTTGCTTATTCGAAACCAAGAGATCTACTCCCAACATCCAT 110  
DB 53779 TCCACTACTGATGCTTCTCTCTGCAAGCAAGCTTGAATGTCACACACACACA 53838

QY 111 CTTACTCATGCACTTCATGCAACGACGACATATGTTTC 151  
DB 53839 CACACACACACACACACACACACACACAAAGCTTGCGCTC 53879

## RESULT 15

US-10-317-273-11  
Sequence 11, Application US/10317273  
Publication No. US20040110158A1  
GENERAL INFORMATION:  
APPLICANT: Kenneth W. Dobie  
TITLE OF INVENTION: MODULATION OF MITOCHONDRIAL RIBOSOMAL PROTEIN L13 EXPRESSION  
FILE REFERENCE: RTS-0478  
CURRENT APPLICATION NUMBER: US/10/317,273  
CURRENT FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 159  
SEQ ID NO 11  
LENGTH: 52001  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 11121, 11122, 11123, 11124, 11125, 11126, 11127, 11128, 11129,  
LOCATION: 11130, 11131, 11132, 11133, 11134, 11135, 11136, 11137,  
LOCATION: 11138, 11139, 11140, 11141, 11142, 11143, 11144, 11145,  
LOCATION: 11146, 11147, 11148, 11149, 11150, 11151, 11152, 11153  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 11154, 11155, 11156, 11157, 11158, 11159, 11160, 11161, 11162,  
LOCATION: 11163, 11164, 11165, 11166, 11167, 11168, 11169, 11170,  
LOCATION: 11171, 11172, 11173, 11174, 11175, 11176, 11177, 11178,  
LOCATION: 11179, 11180, 11181, 11182, 11183, 11184, 11185, 11186  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 11187, 11188, 11189, 11190, 11191, 11192, 11193, 11194, 11195,  
LOCATION: 11196, 11197, 11198, 11199, 11200, 11201, 11202, 11203,  
LOCATION: 11204, 11205, 11206, 11207, 11208, 11209, 11210, 11211,  
LOCATION: 11212, 11213, 11214, 11215, 11216, 11217, 11218, 11219  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 11220  
OTHER INFORMATION: n = A,T,C or G  
US-10-317-273-11

Query Match 19.4%; Score 30.4; DB 7; Length 52001;  
Best Local Similarity 61.2%; Pred. No. 39;  
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 50 TTCATGCTGCAAGCCTTGCTTATTCGAAACCAAGAGATCTACTCCCAACATCCA 109  
DB 20055 TTCTTTTCTAAACGAAATCCATGAAAGAGATATATTTAAACTACCA 20114

QY 110 TCTTACTCATGCAACTTCCA 129  
DB 20115 TCTTTTCAGCAAACTTCTA 20134



US-09-925-065A-778732/c  
; Sequence 778732, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; Nucleotide Polymorphisms in the Human Genome  
; CURRENT APPLICATION NUMBER: US/09/925, 065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243, 096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252, 147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250, 092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261, 766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289, 846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 778732  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-778732

Query Match 19.6%; Score 30.8; DB 6; Length 601;

Best Local Similarity 52.3%; Pred. No. 4.3;  
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 12 ACATGGCATACATCTGTTCAACCGTTCGTTGTCATCGTCAAGCCTTGCCT 71  
DB 354 ACATAGACACTTATTTATTTGTTACTGTTGTCATTTAGATTTTAACTTCCCT 295  
QY 72 ATTGTGACCAAGATGATCTACTCCCAACATTCATCTTACTGCACTTCATG 111  
DB 294 ATTATTAATATTAATTTTCTATACATACATGTTTCTACCATATTTATCTTCTA 235  
QY 132 CAACACGCA 141  
DB 234 AACACTGACA 225

## RESULT 3

US-11-117-187-185  
; Sequence 185, Application US/11117187  
; Publication No. US2005026560A1  
; GENERAL INFORMATION:  
; APPLICANT: PREUSS, DAPHNE  
; APPLICANT: COPELAVVER, GREGORY  
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS  
; FILE REFERENCE: ARCD-303US  
; CURRENT APPLICATION NUMBER: US/11/117, 187  
; CURRENT FILING DATE: 2005-04-28  
; PRIOR APPLICATION NUMBER: US/09/531, 120  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/125, 219  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 185  
; LENGTH: 64415  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (9960)..(21146)  
; OTHER INFORMATION: N = A, C G, or T/U  
US-11-117-187-185

Query Match 19.5%; Score 30.6; DB 12; Length 64415;

Best Local Similarity 58.1%; Pred. No. 20;  
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
QY 65 CTGGCTATCTGAAACCAAGAGATACCTACCTCCCAACATCATCTTATCATGCAAC 124  
DB 7117 CTTCCTCTTTAGATATTAATATTTGCTCTTAAACATTAACCTTAACCTTACAC 7176  
QY 125 TTCATGCAACACGACATATGTTCTGTAAC 157  
DB 7177 TTAAATCCCAACCCCTAAATCTAATCTTAAAC 7209

## RESULT 4

US-11-121-086-13/c  
; Sequence 13, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121, 086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567, 570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13  
; LENGTH: 191797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-13

Query Match 19.4%; Score 30.4; DB 12; Length 191797;

Best Local Similarity 57.3%; Pred. No. 32;  
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 55 TCGTCAAGCTTGGCTTATTTGAAACCAAGAGATACCTACTCCCAACATTCATCTTA 114  
DB 162845 TCCTCCAGATCGCTCTTATTTGAATATATTAACGCTTACACACAAACACTCATATA 162786  
QY 115 CTCATGCACTTCATGCAACACGACATATGTT 150  
DB 162785 TCCATTTTACTCCACACACACACATTTT 162750

## RESULT 5

US-09-925-065A-153052  
; Sequence 153052, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; Nucleotide Polymorphisms in the Human Genome  
; CURRENT APPLICATION NUMBER: US/09/925, 065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243, 096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252, 147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250, 092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261, 766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289, 846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 153052  
; LENGTH: 436  
; TYPE: DNA  
; ORGANISM: Homo sapiens

Query Match 19.5%; Score 30.6; DB 12; Length 64415;

US-09-925-065A-153052

Query Match 19.0%; Score 30.2; DB 6; Length 436;  
Best Local Similarity 60.2%; Pred. No. 6.1;  
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

DB 4 GTCATCTACATGACATGATCTGTTGTAACCCCTGCTGTTGTCATGTCATGCA 63  
256 GGCCTCTGCTTGGAGAGCCCATGCTGTTAACGCCCTCTGCTGCTGCTGTAAT 315

QY 64 CCTTCCCTATTCGACCAAGAG 86  
DB 316 TATATATATTTTGAACAGAG 338

## RESULT 6

US-09-925-065A-285326  
; Sequence 285326, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 285326  
; LENGTH: 617  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-285326

Query Match 19.0%; Score 29.8; DB 6; Length 617;  
Best Local Similarity 60.5%; Pred. No. 9;  
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 74 TCTGAACCAAGAGATCTCTACCTCCCAACATCTCTTACTGCAACTTCATGCA 133  
DB 373 TGTGTGAATTTATATACATCTTCCAAACATCCAGGTTTGTAGCACTTATACCC 432  
QY 134 AACACGACATATGTTCTTG 154  
DB 433 TACCTGACCTRAAGTTAATG 453

## RESULT 7

US-09-925-065A-285327  
; Sequence 285327, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 285327  
LENGTH: 617  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-285327

Query Match 19.0%; Score 29.8; DB 6; Length 617;  
Best Local Similarity 60.5%; Pred. No. 9;  
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 74 TCTGAACCAAGAGATCTCTACCTCCCAACATCTCTTACTGCAACTTCATGCA 133  
DB 373 TGTGTGAATTTATATACATCTTCCAAACATCCAGGTTTGTAGCACTTATACCC 432  
QY 134 AACACGACATATGTTCTTG 154  
DB 433 TACCTGACCTRAAGTTAATG 453

## RESULT 8

US-09-925-065A-285328  
; Sequence 285328, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 285328  
; LENGTH: 617  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-285328

Query Match 19.0%; Score 29.8; DB 6; Length 617;  
Best Local Similarity 60.5%; Pred. No. 9;  
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 74 TCTGAACCAAGAGATCTCTACCTCCCAACATCTCTTACTGCAACTTCATGCA 133  
DB 373 TGTGTGAATTTATATACATCTTCCAAACATCCAGGTTTGTAGCACTTATACCC 432  
QY 134 AACACGACATATGTTCTTG 154  
DB 433 TACCTGACCTRAAGTTAATG 453

## RESULT 9

US-09-925-065A-12385  
; Sequence 12385, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12385  
LENGTH: 1363  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-12385

Query Match 19.0%; Score 29.8; DB 6; Length 1363;  
Best Local Similarity 50.3%; Pred. No. 11;  
Matches 73; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 6 CACTCAGCATGCTACTGCTTTCACCGTTCGCTTTCATCGCCAGCC 65  
DB 765 CACCGACCTGGCCAGTATCAGTTCCTTACCATGTCAGTCTTAAAGTCTTCTG 824  
QY 66 TTGCCTATTTGGAACAGAGATACCTACTCCCAACATCACTTACTCATGCACT 125  
DB 825 TGTGTCTTCTGCGCATGATGTACAGAAAAAAGATCGCTATATATGCACTT 884  
QY 126 TCCATGCAACACGACATATGTTT 150  
DB 885 GAGATGGGAAATTCAGTACGTGT 909

RESULT 10  
US-11-117-187-209/c  
Sequence 209, Application US/11117187  
Publication No. US20050266560A1  
GENERAL INFORMATION:  
APPLICANT: PREUSS, DAPHNE  
APPLICANT: COBENHAVER, GREGORY  
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS  
FILE REFERENCE: ACD:309US  
CURRENT APPLICATION NUMBER: US/11/117,187  
CURRENT FILING DATE: 2005-04-28  
PRIOR APPLICATION NUMBER: US/09/531,120  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 60/125,219  
PRIOR FILING DATE: 1999-03-18  
NUMBER OF SEQ ID NOS: 212  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 209  
LENGTH: 611587  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-11-117-187-209

Query Match 18.7%; Score 29.4; DB 12; Length 611587;  
Best Local Similarity 52.0%; Pred. No. 91;  
Matches 66; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 8 TCTCAGATGGATCTACTGCTTGTTCACCGTTCGCTTGTTCATCGCCAGCCTT 67  
DB 270144 TCTCTCTGCCAGCGATGATTTGTTCATGCACTTTGTGTAACTGCCGACACACTG 270085  
QY 68 GCCTATTCTGAACAGAGATACCTACTCCCAACATCAATCATCTTACTATGCACTTC 127

DB 270084 GCTTGTAGAAAAAACCCCTTTCTTCTTATGAAATGTTGCTTACTCTGTCACTGC 270025  
QY 128 CATGCA 134  
DB 270024 GATACAA 270018

RESULT 11  
US-09-925-065A-805392  
Sequence 805392, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 805392  
LENGTH: 544  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-805392

Query Match 18.3%; Score 28.8; DB 6; Length 544;  
Best Local Similarity 69.6%; Pred. No. 18;  
Matches 39; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 71 TATTTGAACCAAGAGATACCTACTCCCAACATCACTTACTCATGCACTT 126  
DB 23 TATTTAGAAAAAAGAAAAAACCAAAAAATCACTTCCAAATGCAACTT 78

RESULT 12  
US-10-750-185-47517  
Sequence 47517, Application US/10750185  
Publication No. US2005026603A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFIELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 47517  
LENGTH: 1370  
TYPE: DNA  
ORGANISM: Bovine  
US-10-750-185-47517

Query Match 18.3%; Score 28.8; DB 8; Length 1370;

```
Best Local Similarity 54.8%; Pred. No. 24;
Matches 57; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 47 TTGTTTCATGCTGCAAGCTTGTCTTATTCGACCAAGATTAATCTCCAAACAT 106
DB 660 TTGTTTCATGCTGCTGCGCTCCCAATTCAGGAGCTGAGAACTCTGAAATTTAT 719
DB 107 CCATCTTACTGATGCAACTTTCATGCAACAGCAATATGTTT 150
DB 720 CCTGTGCACTGAGAAATGTGACAGAAATGCAAAATGTTT 763

RESULT 13
US-10-750-623-47517
; Sequence 47517, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47517
; LENGTH: 1370
; TYPE: DNA
; ORGANISM: Bovine 1986680570548
US-10-750-623-47517

Query Match 18.3%; Score 28.8; DB 8; Length 1370;
Best Local Similarity 54.8%; Pred. No. 24;
Matches 57; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 47 TTGTTTCATGCTGCAAGCTTGTCTTATTCGACCAAGATTAATCTCCAAACAT 106
DB 660 TTGTTTCATGCTGCTGCGCTCCCAATTCAGGAGCTGAGAACTCTGAAATTTAT 719
QY 107 CCATCTTACTGATGCAACTTTCATGCAACAGCAATATGTTT 150
DB 720 CCTGTGCACTGAGAAATGTGACAGAAATGCAAAATGTTT 763

RESULT 14
US-09-925-065A-845392
; Sequence 845392, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 845392
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-845392

Query Match 18.1%; Score 28.4; DB 6; Length 628;
Best Local Similarity 54.9%; Pred. No. 25;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 30 TTGTTCAACCGTTCGCTTGTTCATGTCAGAGCTTGTCTTATTCGACCAAGAGAT 89
DB 495 TGGTGTGCGCTTCAGATGATGAGTCTTGTAGACTGTGATTAAGTGTGGGCT 554
QY 90 ACCTACTCCCAACATCAATCTTACTATGCAACTTCGATG 131
DB 555 CCCCACTGCCCACTCTCTCTCTGCTGCTGCTTGCATG 596

RESULT 15
US-09-925-065A-33976/C
; Sequence 33976, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33976
; LENGTH: 1691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-33976

Query Match 18.1%; Score 28.4; DB 6; Length 1691;
Best Local Similarity 54.9%; Pred. No. 34;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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QY 90 ACCTACTCCCAACATCAATCTTACTATGCAACTTCGATG 131
DB 1131 CCCCACTGCCCACTCTCTCTCTGCTGCTGCTTGCATG 1090

Search completed: March 6, 2006, 10:32:44
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## RESULT 2

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LOCUS Male tissue-preferred regulatory region and method of using same.
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ACCESSION BD062177
VERSION BD062177.1 GI:22607782
KEYWORDS JP 2001520523-A/2.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 1394)
AUTHORS Albertsen, M. C., Fox, T. W., Garneau, C. W., Huffman, G. A. and Kendall, T. L.
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TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: JP 2001520523-A 2 30-OCT-2001;
PIONEER HI BRED INTERNATIONAL INC
PN JP 2001520523-A/2
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COMMENT PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
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PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNEAU, GARY A HUFFMAN,
PI TIMMY L KENDALL
PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC
, C07K14/34, C12Q1/68,
PC A01H5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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## FEATURES

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7,2e-228; Indels 0; Gaps 0;
Matches 1311; Conservative 0; Mismatches 0;
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RESULT 5  
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LOCUS Zee mays male fertility protein (Me45) gene, complete cds.  
DEFINITION AF360356  
ACCESSION AF360356.1 GI:14028756  
KEYWORDS  
SOURCE Zee mays  
ORGANISM Zee mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 3343)  
AUTHORS Fox,T.W., Trimnell,M.R. and Albertsen,M.C.  
TITLE Cloning of Me45, a gene required for male fertility from Zea mays  
JOURNAL 2 (bases 1 to 3343)  
REFERENCE Fox,T.W., Trimnell,M.R. and Albertsen,M.C.  
AUTHORS Direct Submission  
TITLE Submitted (13-MAR-2001) Trait and Technology Development, Pioneer  
JOURNAL Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,  
IA 50131-1004, USA  
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Best Local Similarity 100.0%; Pred. No. 6,2e-228;  
Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DEFINITION Sequence 9 from Patent WO0160997.
ACCESSION AX224402
VERSION AX224402.1 GI:15554644
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
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Qy 1265 CTTACTGATGCAACTTCATGCAACGACGACATATGTTCTGTAAC 1311
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DEFINITION Sequence 3 from Patent WO0160997.
ACCESSION AX224396
VERSION AX224396.1 GI:15554638
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)
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DEFINITION Zea mays strain B73 clone ZM8Bc0196114, *** SEQUENCING IN PROGRESS
LOCUS AC155584
ACCESSION AC155584.2 GI:58082443
VERSION HTG: HTGS_PHASE1.
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 188283)
AUTHORS Chan,A.P., Percea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Uterback,T.R., Feldblum,T.V., Rabnowicz,P., Fraser,C.M.,
Schubert,K., Samiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Bridman,A., Bedell,J.A., Lakey,N., Barzduk,B., Bennetzen,J. and
Quackenbush,J.
TITLE Consortium for Maize Genomics - BAC skin sequencing and assembly
JOURNAL Unpublished
AUTHORS Chan,A.P., Percea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Uterback,T.R., Feldblum,T.V., Rabnowicz,P., Fraser,C.M.,
Schubert,K., Samiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Bridman,A., Bedell,J.A., Lakey,N., Barzduk,B., Bennetzen,J. and
Quackenbush,J.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 188283)
AUTHORS Chan,A.P., Percea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Uterback,T.R., Feldblum,T.V., Rabnowicz,P., Fraser,C.M.,
Schubert,K., Samiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Bridman,A., Bedell,J.A., Lakey,N., Barzduk,B., Bennetzen,J. and
Quackenbush,J.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57863105.
COMMENT
----- Trace submission
Center name: TIGR
Seq lib id: ZGFX
----- Project information
Web site: http://www.tigr.org/cdb/cgi/maize/
Contact: maize@tigr.org

*****
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
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\* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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22233: gap of unknown length
22234: contig of 5731 bp in length
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35260: contig of 14494 bp in length
49755: gap of unknown length
49855: contig of 46647 bp in length
49856: gap of unknown length
96502: contig of 2074 bp in length
96503: gap of unknown length
98775: gap of unknown length
104000: contig of 5224 bp in length
104100: gap of unknown length
123477: contig of 19378 bp in length
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126564: gap of unknown length
134044: contig of 7480 bp in length
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142805: contig of 8660 bp in length
142806: gap of unknown length
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161077: contig of 1009 bp in length
162086: gap of unknown length
162185: contig of 5320 bp in length
167406: gap of unknown length
167505: contig of 4000 bp in length
171506: gap of unknown length
171605: contig of 1639 bp in length
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/estimated_length=unknown

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gap 159717..159816
gap /estimated_length=unknown
gap 160977..161076
gap /estimated_length=unknown
gap 162086..162185
gap /estimated_length=unknown
gap 167406..167505
gap /estimated_length=unknown
gap 171506..171605
gap /estimated_length=unknown
gap 173245..173344
gap /estimated_length=unknown
gap 184424..184523
gap /estimated_length=unknown

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## ORIGIN

Query Match 5.9%; Score 77.2; DB 14; Length 188283;  
 Best Local Similarity 80.5%; Pred. No. 0.00021;  
 Matches 103; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

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Oy 789 TTTTAAAGACTGTTTGGCAACCTGTTCTTTCAAGATTTGATTTTCAAAA 848
Db 35512 TTTTAAAGGCTAGTTTAAAGACCTGTT--TTTAAAGGATTTTATTTTCTTAAGAG 35569
Oy 849 AAATGATTTTCTTTCTTTTAAATAGAAAACCTTAGAAAATAGAGTCCGAC 908
Db 35570 AAATGATTTTCTTTCTTTTAAATAGAAAATAGAAAATAGTCCGAC 35629
Oy 909 TAGCCCTA 916
Db 35630 TAGCCCTA 35637

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RESULT 9
AC147602 186139 bp DNA linear HTG 17-AUG-2004
LOCUS Zea mays clone ZMMBC0334A01, *** SEQUENCING IN PROGRESS ***
DEFINITION ordered pieces.
ACCESSION AC147602.5 GI:51315585
VERSION HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

```

```

REFERENCE 1 (bases 1 to 186199)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.
and Messing,J.
Ze mays, clone ZMMBC0334A01
JOURNAL Unpublished
2 (bases 1 to 186199)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.
and Messing,J.
Ze mays, clone ZMMBC0334A01

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS

```

Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K. and Messing,J.  
 Ze mays, clone ZMMBC0334A01  
 Unpublished  
 2 (bases 1 to 186199)  
 Anderson,M., Arachchi,H.M., Barua,N., Bastien,V., Bloom,T., Boguslavsky,I., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeRellano,J., Fato,S., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,K., Fero,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagois,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatae,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., Maclean,C., Macdonald,P., Major,J., Manning,J., Mathews,C., McCarthy,M., Meidrum,J., Menes,L., Mihova,T., Mieng,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Riese,C., Rogov,Roman,J., Schaner,S., Schnupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Strange-Rhmann,N., Stojanovic,N., Stubbs,M., Talmeir,T., Tesfaye,S., Theodore,J., Topman,K., Travers,M., Vasiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission



Assembly program: XGAP4, version 4.5  
 Chemistry: Dye-terminator; 100% of reads  
 Consensus quality: 156361 bases at least Q40  
 Consensus quality: 157330 bases at least Q30  
 Consensus quality: 158179 bases at least Q20  
 Insert size: 160416; sum-of-contigs  
 Insert size: 160313; 4.7% error; agarose-fp  
 Quality coverage: 6.55x in Q20 bases; sum-of-contigs Quality  
 coverage: 6.56x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 13 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 3158: contig of 3158 bp in length  
 \* 3159 3258: gap of 100 bp  
 \* 3259 11860: contig of 8602 bp in length  
 \* 11861 11960: gap of 100 bp  
 \* 11961 21800: contig of 9840 bp in length  
 \* 21801 21900: gap of 100 bp  
 \* 21901 45034: contig of 23134 bp in length  
 \* 45035 45134: gap of 100 bp  
 \* 45135 47371: contig of 2237 bp in length  
 \* 47372 47471: gap of 100 bp  
 \* 47472 66727: contig of 19256 bp in length  
 \* 66728 66827: gap of 100 bp  
 \* 66828 79067: contig of 12240 bp in length  
 \* 79068 79167: gap of 100 bp  
 \* 79168 97393: contig of 18226 bp in length  
 \* 97394 97494: gap of 100 bp  
 \* 97494 103542: contig of 6049 bp in length  
 \* 103543 103642: gap of 100 bp  
 \* 103643 112675: contig of 9033 bp in length  
 \* 112676 112775: gap of 100 bp  
 \* 112776 137298: contig of 24523 bp in length  
 \* 137299 137399: gap of 100 bp  
 \* 137399 158790: contig of 21392 bp in length  
 \* 158791 158890: gap of 100 bp  
 \* 158891 161616: contig of 2726 bp in length.

## FEATURES

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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKF1-91021"  
 /clone\_id="DarioKey"  
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 1. 3158  
 /note="assembly fragment:00020  
 fragment chain:1"  
 misc\_feature  
 3259. 11860  
 /note="assembly fragment:00240  
 fragment chain:1"  
 misc\_feature  
 11961. 21800  
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 fragment chain:1"  
 misc\_feature  
 21901. 45034  
 /note="assembly fragment:01299  
 fragment chain:1"  
 misc\_feature  
 45135. 47371  
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 fragment chain:1"  
 misc\_feature  
 47472. 66727  
 /note="assembly fragment:00606  
 fragment chain:1"  
 misc\_feature  
 66828. 79067  
 /note="assembly fragment:00463  
 fragment chain:1"  
 misc\_feature  
 79168. 97393  
 /note="assembly fragment:00794

misc\_feature  
 97494. 103542  
 /note="assembly fragment:00074  
 fragment chain:1"  
 misc\_feature  
 103643. 112675  
 /note="assembly fragment:00146  
 fragment chain:1"  
 misc\_feature  
 112776. 137298  
 /note="assembly fragment:01585  
 fragment chain:1"  
 misc\_feature  
 137399. 158790  
 /note="assembly fragment:01032  
 fragment chain:1"  
 misc\_feature  
 158891. 161616  
 /note="assembly fragment:00044.0"

## ORIGIN

Query Match 5.7%; Score 74.4; DB 14; Length 161616;  
 Best Local Similarity 47.9%; Pred. No. 0.00071;  
 Matches 184; Conservative 0; Mismatches 200; Indels 0; Gaps 0;  
 Oy 576 TTACAAACATCTAGAGGAGCAAAATATATGAAAGGTAGCTAGCTGACATTTT 635  
 Db 79191 TTATTAATAATNNNNAAAAAATATATATAAATTTTNNNTNNTNNTAATTAAT 79250  
 Oy 636 TCTTTTCATCTGTTATTTGTTATGTTTATATATATATATATATATATATATAT 79310  
 Db 79251 TATTTTATTTTATTTTATTTTATATATATATATATATATATATATATATAT 79310  
 Oy 696 AGTGATTTCTGCGATTTTAAATGATCTAAAGTATTTTATATATAGACAGCA 755  
 Db 79311 TTTATATTTTAT 79370  
 Oy 756 TGTCGTAGATTCGCTGCAAAATCTTCGATTTTAAAGCTAGCTTGGCAACCT 815  
 Db 79371 ATTAATAATTTTNNAAAAATTTTNTTTTATATATATATATATATATATAT 79430  
 Oy 816 GTTTCCTTCAAGATTTTGATTTTTCAAAAAATTAAGTATTTTCTCTATATAA 875  
 Db 79431 TTTATATTTAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 79490  
 Oy 876 TACAAACACTTAGAAAAATAGAGTCCAGACTAGCCCTAGAAAGTTTCCCAATAAT 935  
 Db 79491 TNNAAAAAT 79550  
 Oy 936 TACAATCACTGTGATATATATTTT 959  
 Db 79551 ATATATATATATATATATTTT 79574

RESULT 11  
 AC117267 25769 bp DNA linear INV 21-FEB-2004  
 LOCUS  
 DEFINITION  
 Dictyostelium discoideum chromosome 2 map 5816255-5862024 strain  
 AX4, complete sequence.  
 ACCESSION  
 AC117267 AC115597  
 VERSION  
 AC117267.2 GI:42733680  
 KEYWORDS  
 HTG.  
 SOURCE  
 Dictyostelium discoideum  
 ORGANISM  
 Dictyostelium discoideum  
 Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
 1 (bases 1 to 25769)  
 Gloeckner G., Eichinger L., Szafrenski K., Pachebat D., Dear P.,  
 Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,  
 Jungel B., Cox E., Quail M.A., Platzer M., Rosenthal A. and  
 Noegel A.A.  
 Sequence and analysis of chromosome 2 of Dictyostelium discoideum  
 NATURE 418 (6893), 79-85 (2002)  
 JOURNAL  
 NATURE 418 (6893), 79-85 (2002)  
 PUBMED  
 12097910  
 REMARK  
 The Dictyostelium Genome Sequencing Consortium  
 2 (bases 1 to 25769)  
 REFERENCE  
 Baumgart C.  
 DIRECT SUBMISSION





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* 66377 70448: contig of 4072 bp in length
* 70449 gap of unknown length
* 70549 74167: contig of 3619 bp in length
* 74168 74267: gap of unknown length
* 74268 82175: contig of 7908 bp in length
* 82176 82275: gap of unknown length
* 82276 83496: contig of 1221 bp in length
* 83497 83596: gap of unknown length
* 114545 114644: contig of 30948 bp in length
* 114545 116257: contig of 1613 bp in length
* 116358 116357: gap of unknown length
* 116358 119322: contig of 2965 bp in length
* 119323 119422: gap of unknown length
* 119423 121368: contig of 1946 bp in length
* 121369 121468: gap of unknown length
* 121469 125359: contig of 3391 bp in length
* 125360 125459: gap of unknown length
* 125460 126905: contig of 1446 bp in length
* 126906 131580: contig of 4575 bp in length
* 131581 131680: gap of unknown length
* 131681 134564: contig of 2884 bp in length
* 134565 134664: gap of unknown length
* 134665 138587: contig of 3923 bp in length
* 138588 138687: gap of unknown length
* 138688 156638: contig of 17951 bp in length
* 156639 156738: gap of unknown length
* 156739 167111: contig of 10373 bp in length
* 167112 167211: gap of unknown length
* 167212 168221: contig of 1010 bp in length
* 168222 168321: gap of unknown length
* 168322 172293: contig of 3972 bp in length.

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## FEATURES

## SOURCE

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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBB0131C15"
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5335..5434
/estimated_length=unknown
8099..8196
/estimated_length=unknown
10615..10714
/estimated_length=unknown
12842..12941
/estimated_length=unknown
15186..15285
/estimated_length=unknown
36328..36427
/estimated_length=unknown
44530..44629
/estimated_length=unknown
58059..58158
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66277..66376
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74168..74267
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82176..82275
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83497..83596
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/estimated_length=unknown
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119323..119422

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/estimated_length=unknown
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/estimated_length=unknown
125360..125459
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126906..127005
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131581..131680
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134565..134664
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138588..138687
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168222..168321
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## ORIGIN

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Query Match 5.5%; Score 72.4; DB 14; Length 172293;
Best Local Similarity 78.6%; Pred. No. 0.0016;
Matches 99; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

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Qy 791 TTTTAAGCTAGTTGGCAACCTGTTCTTCAAGAATTTGATTTTTCAAAAA 850
Db 27185 TGTTAAGCTAGTTGGCAACCTGTTCTTCAAGAATTTTCCCAAGGAAA 27127
Qy 851 ATTAGTTATTTTCTCTTTTAAATAGAAAACACTTGAAGTTGCGACACTA 910
Db 27126 ATTAGTTATTTTCTCTTTTAAATAGAAAACACTTGAAGTTGCGACACTA 27067
Qy 911 GCCCTA 916
Db 27066 GCCCTA 27061

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## RESULT 13

## AC155618/c

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LOCUS 201985 bp DNA linear HTG 25-JAN-2005
DEFINITION Zea mays strain B73 clone ZMMBB0344D04, *** SEQUENCING IN PROGRESS
ACCESSION AC155618
VERSION AC155618.2 GI:58082477
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Zea mays

```

## ORGANISM

```

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 201985)

```

## REFERENCE

## AUTHORS

```

Chan, A.P., Perrea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Uteirack, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., Sam Miguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.

```

```

Consortium for Maize Genomics - BAC skim sequencing and assembly
unpublished
2 (bases 1 to 201985)

```

## TITLE

## JOURNML

## AUTHORS

```

Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 201985)
Chan, A.P., Perrea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Uteirack, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., Sam Miguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.

```

## REFERENCE

## AUTHORS

```

Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 201985)
Chan, A.P., Perrea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Uteirack, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., Sam Miguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.

```

TITLE  
JOURNAL  
COMMENT

Quackenbush, J.  
Direct Submission  
Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR)  
9712 Medical Center Dr, Rockville, MD 20850  
On Jan 25, 2005 this sequence version replaced gi:57863139.

Center name: TIGR  
Seq\_id: Z63W

Project information  
Web site: http://www.tigr.org/cdb/cgi/maize/  
Contact: maize@tigr.org

NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1916: contig of 1916 bp in length  
1 1917: gap of unknown length  
1 2017: gap of unknown length  
1 22480: contig of 20464 bp in length  
1 22481: gap of unknown length  
1 22482: gap of 7888 bp in length  
1 30469: gap of unknown length  
1 30469: gap of 34650 bp in length  
1 65319: gap of unknown length  
1 65319: gap of 13456 bp in length  
1 78775: gap of unknown length  
1 78775: gap of 8923 bp in length  
1 87798: gap of unknown length  
1 87798: gap of 6566 bp in length  
1 94464: gap of unknown length  
1 94464: gap of 27198 bp in length  
1 121761: contig of 27198 bp in length  
1 121762: gap of unknown length  
1 124636: contig of 2775 bp in length  
1 124637: gap of unknown length  
1 124737: contig of 6293 bp in length  
1 131029: gap of unknown length  
1 131030: gap of 7610 bp in length  
1 131030: gap of unknown length  
1 138730: gap of 8020 bp in length  
1 138740: gap of unknown length  
1 146860: gap of 6010 bp in length  
1 146860: gap of unknown length  
1 146960: gap of 1957 bp in length  
1 152970: gap of unknown length  
1 153070: gap of 1308 bp in length  
1 155027: gap of unknown length  
1 155127: gap of 16690 bp in length  
1 155127: gap of unknown length  
1 156435: gap of 1534 bp in length  
1 156435: gap of 17324 bp in length  
1 173325: gap of 1534 bp in length  
1 173325: gap of unknown length  
1 174859: gap of 7742 bp in length  
1 174859: gap of unknown length  
1 182701: gap of 3072 bp in length  
1 182801: gap of unknown length  
1 185873: gap of 13529 bp in length  
1 185873: gap of unknown length  
1 193502: gap of 2384 bp in length  
1 193502: gap of unknown length  
1 196602: contig of 2384 bp in length.

# FEATURES

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/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMWBBC014D04"  
1917. 2016  
/estimated\_length=unknown  
22481. 22580  
/estimated\_length=unknown  
30469. 30568  
gap  
gap  
gap

gap /estimated\_length=unknown  
gap 65219..65318 /estimated\_length=unknown  
gap 78775..78874 /estimated\_length=unknown  
gap 87798..87897 /estimated\_length=unknown  
gap 94464..94563 /estimated\_length=unknown  
gap 121762..121861 /estimated\_length=unknown  
gap 124637..124736 /estimated\_length=unknown  
gap 131030..131129 /estimated\_length=unknown  
gap 138740..138839 /estimated\_length=unknown  
gap 146860..146959 /estimated\_length=unknown  
gap 152970..153069 /estimated\_length=unknown  
gap 155027..155126 /estimated\_length=unknown  
gap 156435..156534 /estimated\_length=unknown  
gap 173325..173424 /estimated\_length=unknown  
gap 174859..174958 /estimated\_length=unknown  
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gap 185873..185972 /estimated\_length=unknown  
gap 193502..193601 /estimated\_length=unknown  
gap /estimated\_length=unknown

## ORIGIN

Query Match 5.5%; Score 71.6; DB 14; Length 201985;  
Best Local Similarity 76.9%; Pred. No. 0.0022;  
Matches 100; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 792 TTTAAGAGCTGTTGGACACCGTCTTCAAGATTTGATTTTCAAAAAA 851  
DB 44986 TATTAAGGCTAGTTTGGACACCATATTT-TTCAAGGATTTTCCCAAGAAA 44928  
QY 852 TTTGTTATTTTCTTTTAAATAGAAACCTTAGAAATAGATGCGAGCTAG 911  
DB 44927 TTATGTCATTTTCCATAGAAATAGAAATCCATGGAATATGATTCCTCAACTAG 44868  
QY 912 CCTAGATG 921  
DB 44867 CCTAAAGAAG 44858

RESULT 14  
LOCUS AF034389/c 713 bp DNA linear INV 04-FEB-1999  
DEFINITION Plasmodium falciparum sexual stage antigen (a16) gene, promoter and partial cde.  
ACCESSION AF034389  
VERSION AF034389.1 GI:3098230  
KEYWORDS Plasmodium falciparum (malaria parasite P. falciparum)  
ORGANISM Plasmodium falciparum  
REFERENCE Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
AUTHORS Dehnering K.J., Kaan A.M., Mocham W., Wirth D.F., Eling W., Konings R.N. and Stuenkelberg H.G.  
TITLE Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria parasite Plasmodium falciparum  
JOURNAL Mol. Cell. Biol. 19 (2), 967-978 (1999)  
PUBMED 9891033





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```

Db      1  ACCAGCATGCTAGTGCCTACTATGGCACTACCCAGAACAAATTTAAAAAATAACC 60
Qy      464  AAAATCACTATCCACCTCGAAGCATATCATATGTTTAAAGAAACATCTAATTAACC 523
Db      61  AAAATCACTATCCACCTCGAAGCATATCATATGTTTAAAGAAACATCTAATTAACC 120
Qy      524  ACAGTCCCTTAAACAAACATATTTGAAAGAGCAAAATTAATGTTACAGTTTACAA 583
Db      121  ACAGTCCCTTAAACAAACATATTTGAAAGAGCAAAATTAATGTTACAGTTTACAA 180
Qy      584  CATCTAAGAGGACAAATTAATGAAAGGTAAGCTATGACGTTGACATTTTCTTTTC 643
Db      181  CATCTAAGAGGACAAATTAATGAAAGGTAAGCTATGACGTTGACATTTTCTTTTC 240
Qy      644  ATCTGTGTTATTTGTTATGTTTATATATCATTTTCTCTCTTAAAGTAGAGTAT 703
Db      241  ATCTGTGTTATTTGTTATGTTTATATATCATTTTCTCTCTTAAAGTAGAGTAT 300
Qy      704  TCTTCCGATTTTAAATGAATTAAGTATTTTATATAGAGCAGCATGTCGTAG 763
Db      301  TCTTCCGATTTTAAATGAATTAAGTATTTTATATAGAGCAGCATGTCGTAG 360
Qy      764  ATTCTCGTTCAAAATCTTTCTGATTTTAAAGAGCTAGTTGGCAACCTGTTCTT 823
Db      361  ATTCTCGTTCAAAATCTTTCTGATTTTAAAGAGCTAGTTGGCAACCTGTTCTT 420
Qy      824  CAAAGAAATTTGATTTTTCAAAAAAATTAATGTTATTTCTCTTAAATTAAGAAAC 883
Db      421  CAAAGAAATTTGATTTTTCAAAAAAATTAATGTTATTTCTCTTAAATTAAGAAAC 480
Qy      884  ACTTAGAAAAATAGAGTTGCGACAGTACAGCTAGATGTTTCCCAATTAATTAATCA 943
Db      481  ACTTAGAAAAATAGAGTTGCGACAGTACAGCTAGATGTTTCCCAATTAATTAATCA 540
Qy      944  CTGTGTATTAATTAATTTGGCCAGCCCATTAATTAATTAACCGAAATCGAAGCGA 1003
Db      541  CTGTGTATTAATTAATTTGGCCAGCCCATTAATTAATTAACCGAAATCGAAGCGA 600
Qy      1004  AACCAAACTGAGCAATTTCTGATTAATTAAGGAGGAGAGAGAGGAAAGAAATAG 1063
Db      601  AACCAAACTGAGCAATTTCTGATTAATTAAGGAGGAGAGAGAGGAAAGAAATAG 660
Qy      1064  TTTTAAAGTATGTCCTCGATGATGTCGGTTTGGCAAGATAGCAGCCGTAATCATGCT 1123
Db      661  TTTTAAAGTATGTCCTCGATGATGTCGGTTTGGCAAGATAGCAGCCGTAATCATGCT 720
Qy      1124  CATAGTGCCTAAGTCAAGTTCGCGAGCTCTGTCATCTCAATGCGCATATCAATGC 1183
Db      721  CATAGTGCCTAAGTCAAGTTCGCGAGCTCTGTCATCTCAATGCGCATATCAATGC 780
Qy      1184  TTGTTCAACCGTTCCTGTTTCCATGCTGCAAGCTTGCCATTCGTAACCAAGAGAT 1243
Db      781  TTGTTCAACCGTTCCTGTTTCCATGCTGCAAGCTTGCCATTCGTAACCAAGAGAT 840
Qy      1244  ACTTACTCCCAACATCATCTTACTCATGCAATCTTCATGCAAAACAGCAGCATATGTT 1303
Db      841  ACTTACTCCCAACATCATCTTACTCATGCAATCTTCATGCAAAACAGCAGCATATGTT 900
Qy      1304  TCCTGAAC 1311
Db      901  TCCTGAAC 908

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RESULT 2
CG224225          915 bp   DNA      linear   GSS 22-AUG-2003
LOCUS             OGIAG08TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBma0716B15,
DEFINITION        Genomic survey sequence.
ACCESSION         CG224225.1 GI:34124113
VERSION           GSS.
KEYWORDS           Zea mays
SOURCE

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ORGANISM Zea mays
           Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoidae; Andropogonaceae; Zea.
REFERENCE 1 (bases 1 to 915)
AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
           Resnick,A., Fraser,C.M., Budiman,W.A., Bedell,J.A., Kohlfing,T.,
           Citek,R.W., Nunez,A., Robbins,D., and Lakey,N.
TITLE     Consortium for Maize Genomics
JOURNAL   Unpublished (2002)
COMMENT   Other_GSSs: OGIAG08TV
           Contact: Cathy Whitelaw
           TIGR
           9712 Medical Center Drive, Rockville, MD 20850, USA
           Tel: 301-838-5843
           Fax: 301-838-0208
           Email: whitelaw@tigr.org
           Seq primer: TP
           Class: methylation filtered.
           Location/Qualifiers
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               /mol_type="genomic DNA"
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               /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
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## ORIGIN

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Query Match      51.8%; Score 679; DB 10; Length 915;
Best Local Similarity 99.9%; Pred. No. 9.5e-112;
Matches 690; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      621  TGAGGTTCAAGTTTCTTTTTCATTTCTGTATTTGTTATGTTTATATATCATTTT 680
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Qy      681  CTTCTTCAAAATGAGTGAATTTCTCCGATTTTATTAATGACTTAAGTCAATTTT 740
Db      60  CTTCTTCAAAATGAGTGAATTTCTCCGATTTTATTAATGACTTAAGTCAATTTT 119
Qy      741  ATATAGAGCAGCATGCTGATATCTGTCATAAAATCTTTCTGATTTTATTAAGAGC 800
Db      120  ATATAGAGCAGCATGCTGATATCTGTCATAAAATCTTTCTGATTTTATTAAGAGC 179
Qy      801  TAGTTTGGCAACCTGTTTCTTTCAAGAAATTTGATTTTCAAAAAAATTAAGTTAT 860
Db      180  TAGTTTGGCAACCTGTTTCTTTCAAGAAATTTGATTTTCAAAAAAATTAAGTTAT 239
Qy      861  TTCTCTTTTAAATTAAGAAACCTTAGAAAAATAGTTGCGAGCTAGCCCTAGAT 920
Db      240  TTCTCTTTTAAATTAAGAAACCTTAGAAAAATAGTTGCGAGCTAGCCCTAGAT 299
Qy      921  GTTTTCCCAATTAATTAATCACTGCTGATTAATTAATTTGCGCAGCCCAATTAATTT 980
Db      300  GTTTTCCCAATTAATTAATCACTGCTGATTAATTAATTTGCGCAGCCCAATTAATTT 359
Qy      981  AAACCGAAATCTGAATGAGGGAACCAATCTAGCTATTTCTCTGATTAATTAAG 1040
Db      360  AAACCGAAATCTGAATGAGGGAACCAATCTAGCTATTTCTCTGATTAATTAAG 419
Qy      1041  GGAGAGAGAGGGAAGAAATGATTTAAGTATGTCCTGAGATGCGGTTGGCAA 1100
Db      420  GGAGAGAGAGGGAAGAAATGATTTAAGTATGTCCTGAGATGCGGTTGGCAA 479
Qy      1101  CGATAGCAGCAGTATATAGTCTATAGTGCCTACGTCAGTTCGCGAGCTCTGTC 1160
Db      480  CGATAGCAGCAGTATATAGTCTATAGTGCCTACGTCAGTTCGCGAGCTCTGTC 539
Qy      1161  ATCTCAATGGCATATCAATGCTGTTGTTCAACGTTGCTGTTGTTCAATGCTCAAGCCT 1220

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Db 540 ATCTGACATGACATGCTGTTGTCACCGTTGCTGTTTCATGCTCCAGCCT 599  
Qy 1221 TGGCATTCGACACGAGATGATCCATCCCAAGATCATCTGTCAGCACTT 1280  
Db 600 TGGCATTCGACACGAGATGATCCATCCCAAGATCATCTGTCAGCACTT 659  
Qy 1281 CCGTCAACACGACATGTTGTTCCGTAAC 1311  
Db 660 CCGTCAACACGACATGTTGTTCCGTAAC 690

RESULT 3  
CC656939/c 687 bp DNA linear GSS 19-JUN-2003  
LOCUS OGM020TV.ZM.0.7.1.5.KB Zea mays genomic clone ZMMBMA0554D15,  
DEFINITION genomic survey sequence.  
ACCESSION CC656939  
VERSION CC656939.1 GI:32060231  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 687)  
White, C.A., Quackenbush, J., Van Aken, S., Utecher, T.,  
Rennick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunez, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGM020TV  
Contact: Cathy Whitelaw  
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TP  
Class: methylation filtered.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
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Best Local Similarity 99.5%; Pred. No. 2e-77;  
Matches 421; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 889 GAAAAATAGAGTTGACAGACTAGCCCTGAAATGTTTCCCAATTAATCAATCACTGTG 948  
Db 687 GAAAAATAGAGTTGACAGACTAGCCCTGAAATGTTTCCCAATTAATCAATCACTGTG 628  
Qy 949 TATATATTTTGGCAGCCGCCATTAATTTTAAACCGAACTGAATGACCGAAACCA 1008  
Db 627 TATATATTTTGGCAGCCGCCATTAATTTTAAACCGAACTGAATGACCGAAACCA 568  
Qy 1009 AATGAGCTATTTCTGATAGTAATTAAGGAGAGAGAGAGAGAAATCAATTTTA 1068  
Db 567 AATGAGCTATTTCTGATAGTAATTAAGGAGAGAGAGAGAGAAATCAATTTTA 508  
Qy 1069 AGCATATGCTGAG 1128  
Db 507 AGCATATGCTGAG 448  
Qy 1129 GTGCTTGTGAGTTGGCAGCTCTGCTGATCTGATGAGATGAGATGAGATGAGTTT 1188

Db 447 GTGCTTGTGAGTTGGCAGCTCTGCTGATCTGATGAGATGAGATGAGTTT 388  
Qy 1189 CAACGCTTGTGAGTTGGCAGCTCTGATGAGATGAGATGAGATGAGTTT 1248  
Db 387 CAACGCTTGTGAGTTGGCAGCTCTGATGAGATGAGATGAGATGAGTTT 328  
Qy 1249 CTCGCAACATCATCTTACTGATGAGATGAGATGAGATGAGATGAGATGAGTTT 1308  
Db 327 CTCGCAACATCATCTTACTGATGAGATGAGATGAGATGAGATGAGATGAGTTT 268  
Qy 1309 AAC 1311  
Db 267 AAC 265

RESULT 4  
CG252571/c 715 bp DNA linear GSS 25-AUG-2003  
LOCUS OG4B057C.ZM.0.7.1.5.KB Zea mays genomic clone ZMMBMA0809B10,  
DEFINITION genomic survey sequence.  
ACCESSION CG252571  
VERSION CG252571.1 GI:34154661  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 715)  
White, C.A., Quackenbush, J., Van Aken, S., Utecher, T.,  
Rennick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunez, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Contact: Cathy Whitelaw  
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TP  
Class: methylation filtered.  
Location/Qualifiers  
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Best Local Similarity 80.1%; Pred. No. 1.5e-09;  
Matches 125; Conservative 0; Mismatches 30; Indels 1; Gaps 1;  
Qy 135 TCTCCACCTGCGCTGACATCTTGTGATGAGTGTGCTTCCCATGACGAGGCCA 194  
Db 356 TCCACACCTGCGCTGATGAGTGTGCTTGTGATGAGTGTGCTTCCCATGACGAGGCCA 297  
Qy 195 TCAGACCTTGTGAGACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254  
Db 296 TCAGACCTTGTGAGACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 238  
Qy 255 TCGTGTGATCCAGGGGATATATGTCCTCCCAATC 290  
Db 237 TCGTGTGATCCAGGGGATATATGTCCTCCCAATC 202

RESULT 5  
CL235046

LOCUS CL235046 967 bp DNA linear GSS 15-JAN-2004  
DEFINITION ZMMBB0575001r ZMMBB (HindIII) Zea mays genomic clone  
ACCESSION ZMMBB0575001.3, genomic survey sequence.  
VERSION CL235046  
KEYWORDS CL235046.1 GI:40891729  
SOURCE GSS.  
ORGANISM Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 967)  
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.  
TITLE Sequencing of the maize genome at PGR (2003c)  
JOURNAL Unpublished (2003)  
COMMENT Contact: Bharti,A.K.  
Dr.Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: SP6  
Class: BAC ends  
High quality sequence start: 64.  
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Best Local Similarity 78.6%; Pred. No. 1e-08;  
Matches 110; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
OY 150 TGCAACATTTCTGATGTCGATGTTCCCATCTGACGAGGCCCATCAGACCTTTGG 209  
DB 827 TGGCGCTTCTTGATGATACCGCGGCTTCCGCTGATTGAGGCCCATCAGACCTTTGG 886  
OY 210 GACACCCATCAAGGCGCTTTGGATGCGCCACGAGACGTATCGGCTGTGTATCCAG 269  
DB 887 GTGGCCCATCAAGTGCCTTTGCGATGTCACGCGATGTATCCGGCGGTGACCTGG 946  
OY 270 GGATATATGTCGCCCAAT 289  
DB 947 GGATATCTGTCCCATAGT 966

RESULT 6  
LOCUS C2295176 860 bp DNA linear GSS 23-MAR-2005  
DEFINITION ZMMBF0063M20f ZMMBF Zea mays genomic clone ZMMBF0063M20 5', genomic  
survey sequence.  
ACCESSION C2295176  
VERSION C2295176.1 GI:61708952  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 860)  
AUTHORS Bharti,A.K., Nelson,A.B., Young,S., Keizer,G., Zohovetz,V., Fuks,G.  
and Messing,J.  
TITLE Construction, Sequencing and Characterization of a Fosmid Library

JOURNAL of the B73 Maize Genome  
COMMENT Unpublished (2005)  
Contact: Bharti,A.K.  
Dr.Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: Fos\_F  
Class: Fosmid ends  
Location/Qualifiers  
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Best Local Similarity 62.6%; Pred. No. 1.7e-08;  
Matches 142; Conservative 0; Mismatches 85; Indels 0; Gaps 0;  
OY 782 TTTCGATTTTATAGAGCTAGTTGGCAACCCGTTCTTCAAGAAATTTGATTTT 841  
DB 51 TTCAAGACCTCTAAGGCGTAGTTGCAACCCATTTTCTAAGAAATTTTATTTT 110  
OY 842 TCAAAAAAATAGTTATTTTCTCTTATTAATAAGAAAAACATTAGAAAAATAGATT 901  
DB 111 TAAAGAAATTAAGTTATTTCTCTCTGTAATGAATCCCTTAAAAAATTAAGTT 170  
OY 902 GCCAGACTAGCCCTAGATGTTTCCCAATTAATTACATCACTGTATTAATTATTTGG 961  
DB 171 ACTAAATTAGCCTTAAAGTTGGTTGATGACCAAAATTAAGTGTAAAGACGA 230  
OY 962 CCAGCCCATTAATTAATTAAACCGAATCGAATCGAGGAACCA 1008  
DB 231 GAATCCCTTCTAATGATGAGGGGAGAGAAATTCGTAACATCA 277

RESULT 7  
LOCUS CG048704 814 bp DNA linear GSS 19-AUG-2003  
DEFINITION PUILO19TB ZM 0.6\_1.0\_KB Zea mays genomic clone ZMMBTA0611C13,  
genomic survey sequence.  
ACCESSION CG048704  
VERSION CG048704.1 GI:33920884  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 814)  
AUTHORS WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Benneetzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUILO19TD  
Contact: Cathy WhiteJaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteJaw@tigr.org  
Seq primer: TK  
Class: sheared ends.

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ORIGIN  
Query Match 6.7%; Score 88; DB 10; Length 814;  
Best Local Similarity 62.7%; Pred. No. 7.1e-08;  
Matches 153; Conservative 0; Mismatches 90; Indels 1; Gaps 1;  
QY 713 TTTATTAATGACTATTAAGTCATTTTATATTAAGACGACGATGTGATGATTCGTT 772  
DB 487 TTTAGAGACGTGTGTGATGATGAGAAATATGAGAAATATCTTTTATGAGATGTA 546  
QY 773 CAAAATCTTTCTGATTTTATTAAGAGCTGTTGGCAACCCGTTCTTTCAAGAT 832  
DB 547 TAAAGACAAAGAACATTTCTTATAGAGCTGTTGGTATCCCATTTTTCAGAGAT 606  
QY 833 TTGATTTTTCAGAAA-AAATATGTTTATTTCTTTATTAATTAAGAAACATTAGAA 891  
DB 607 TTGATTTCTACAGAGGAAATATGTTATTTCCCTTTTGAATGATACGCGAA 666  
QY 892 AAATAGATGTCAGACTAGACCTGAGAAATGTTTCCCATTAATTAATCAATGATGTA 951  
DB 667 AAATAGATTTCTCAATACCTTACGTTATATCCCATATATCCCTATCTCATCTCT 726  
QY 952 AATT 955  
DB 727 ATTT 730

RESULT 8  
CG414922/c 754 bp DNA linear GSS 08-SEP-2003  
LOCUS ZMMBB0290L09.r ZMMBB Zea mays genomic clone ZMMBB0290L09 3'  
DEFINITION genomic survey sequence.  
ACCESSION CG414922  
VERSION CG414922.1 GI:34505144  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 754) Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.  
and Wing, R.  
Sequencing of the maize genome  
Unpublished (2003)  
JOURNAL Contact: Rod Wing  
COMMENT Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: T7  
BACKWARD: M13r  
Plate: 0290 Row: L Column: 09  
Seq primer: M13r  
Class: BAC ends.  
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Best Local Similarity 72.4%; Pred. No. 1.3e-07;  
Matches 126; Conservative 0; Mismatches 47; Indels 1; Gaps 1;  
QY 787 ATTTTATAGAGCTAGTTGGCAACCCGTTCTTTCAAGATTTGATTTTCAAA 846  
DB 241 ATCTTTATAGACTAGTTGGCAACCTTATTT-TCTCAGCGAATTTTATTTTCAAT 183

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Best Local Similarity 71.2%; Pred. No. 7.8e-08;  
Matches 116; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
QY 779 TCTTTGATTTTATTAAGAGCTAGTTGGCAACCCGTTCTTTCAAGATTTGAT 838  
DB 680 TCTAAATTTTCTCAAGCTAGTTTGAAGACATTTTTCAGAGATTTTAA 621  
QY 839 TTTTCAAAAAATATGTTTATTTCTTTTAAATTAAGAAACATTAGAAAAATAGA 898  
DB 620 TTTCTAAATTAATTAATTCATTTTCTTGAATAATTAATCAATGATTAATAA 561  
QY 899 GTTGCAGACTAGCTTACATGTTTCCCATTAATTAATCAAT 941  
DB 560 GTTCTTAATTAATCTTAAATAATTTCTGTCATTAAGCT 518

RESULT 9  
CC439901/c 950 bp DNA linear GSS 20-MAY-2003  
LOCUS PURV15TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBT519D06,  
DEFINITION genomic survey sequence.  
ACCESSION CC439901  
VERSION CC439901.1 GI:30940477  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 950) Whitehead, J., Van Aken, S., Utechtback, T.,  
Whitehead, C.A., Quackenbush, J., Yuan, Y., San Miguel, P., Ma, J. and  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Bennetzen, J.  
Maize Genomics Consortium  
Unpublished (2003)  
JOURNAL Other GSSs: PURV15TD  
COMMENT Contact: Cathy Whitehead  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitehead@tigr.org  
Seq primer: TP  
Class: sheared ends.  
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Db 606 GAAATTTAGTTTATTTCTCTGTGAGAAATATTAATCATCTTGAGAAAAATATAGTTCCAA 547  
Qy 907 ACTAGCCCTAGAAATGTTTCCCAATTAATTAACAATCACTGTATTAATTTG 960  
Db 546 ACTAGCCCTAAGATTTTATTAATAATAGAGAAAAATTCGTCATTTTCATTG 493

Query Match 6.5%; Score 85.2; DB 10; Length 765;  
Best Local Similarity 71.8%; Pred. No. 2.7e-07;  
Matches 125; Conservative 0; Mismatches 48; Indels 1; Gaps 1;

Search completed: March 6, 2006, 01:57:38  
Job time : 6193.32 secs

Qy 787 ATTTTAAAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTTTTCAAA 846  
Db 255 ATCTTCTAATGACTAGTTGGAACTTATTT-TCTCAGCGAGTTTATTTTTCAT 197  
Qy 847 AAAAAATGATTATTTCTCTTATTAATAATAGAAAAACCTAGAAAAATAGATTGCCAG 906  
Db 196 GAAATTTAGTTTATTTCTCTGAGAAATATTAATCATCTTGAGAAAAATATAGTTCCAA 137  
Qy 907 ACTAGCCCTAGAAATGTTTCCCAATTAATTAATCATCTGTATTAATTTG 960  
Db 136 ACTAGCCCTAAGATTTTATTAATAATAGAGAAAAATTCGTCATTTTCATTG 83

RESULT 15  
CC630219/c 781 bp DNA linear GSS 19-JUN-2003

LOCUS OGCUG53TV ZM 0.71.5 KB Zea mays genomic clone ZMMB1a0406J09,  
genomic survey sequence.

ACCESSION CC630219  
VERSION CC630219.1 GI:32003354  
KEYWORDS GSS.

SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 781)  
White, C.A., Quackenbush, J., Van Aken, S., Uteerback, T.,  
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nuneberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)

TITLE JOURNAL  
COMMENT Other\_GSSs: OGCUG53TH  
Contact: Cathy White, law  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: white.law@tigr.org

Class: methylation filtered.  
Location/Qualifiers  
1..781  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMB1a0406J09"  
/clone\_lib="ZM\_0.7\_1.5\_KB"  
/note="Vector: pBCSK-; Site\_1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

FEATURES  
SOURCE

ORIGIN

Query Match 6.5%; Score 85.2; DB 9; Length 781;  
Best Local Similarity 71.8%; Pred. No. 2.7e-07;  
Matches 125; Conservative 0; Mismatches 48; Indels 1; Gaps 1;

Qy 787 ATTTTAAAGAGCTAGTTGGCAACCTGTTCTTCAAGAAATTTGATTTTTCAAA 846  
Db 665 ATCTTCTAATGACTAGTTGGAACTTATTT-TCTCAGCGAGTTTATTTTTCAT 607  
Qy 847 AAAAAATGATTATTTCTCTTATTAATAATAGAAAAACCTAGAAAAATAGATTGCCAG 906



Qy 790 TTTTAAAGCTAGTTGGCAACCCCTGTTCTTTCATGAATTTGATTTTTCAAAAA 849  
Db 511 TTTATTTAGGCTAATTTGGTAACACATTT-TTCACGAAATTTCAATTTTCCATAGGA 569  
Qy 850 AATTAGTTTATTTCTCTTTATTAATAATGAAAAACCTTAGAAAAATGAGTTGCCAGACT 909  
Db 570 AATTAGTTAATTTTCGTTGGGAAAAATGAAATTTCAATGGGAAAAATGCGTTCCCAAACT 629  
Qy 910 AGCCCTAG 917  
Db 630 AGCCTTAG 637

RESULT 2  
US-10-240-708-36  
Sequence 36, Application US/10240708  
Publication No. US20050282157A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENBROCK, Christian  
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
FILE REFERENCE: 5013.1012  
CURRENT APPLICATION NUMBER: US/10/240.708  
PRIOR FILING DATE: 2002-10-03  
PRIOR APPLICATION NUMBER: PCT/EP01/03971  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: DE 10019058.8  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
NUMBER OF SEQ ID NOS: 98  
SEQ ID NO 36  
LENGTH: 9347  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-240-708-36

Query Match 4.4%; Score 57.8; DB 8; Length 9347;  
Best Local Similarity 48.9%; Pred. No. 0.64;  
Matches 155; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

Qy 547 TATTTGAAAGAGCAAAATTTAGTTACAGTTTACAAACATCTAAGAGCGACAAATATAT 606  
Db 8530 TTTTATTTTGTATGAAAGATTTAAATTTTATATATTTAGAGAAATGAATATTTT 8589  
Qy 607 CGAAAGTAGCTATGACGTTCAATTTTCTTTTCACTCTGTTATTTTGTATTTGTT 666  
Db 8590 AAGTATTTTAAATAGATTTTGTATATTTTATTTTATTTTATTTTGTATTTTGT 8649  
Qy 667 TTTATATCATTTTCTCTTCAATAGAGATTTTCTCCGATTTTATAAATGACT 726  
Db 8650 TATTATATTTAATTTATAGTTTTTTATATAGATTTTGTATTTTGTATTTATGATA 8709  
Qy 727 ATAAAGTCATTTTATATAGAGCAGCATGCTAGATTTCTGTTCAAAAATCTTTCTG 786  
Db 8710 TAAATATTTTGTGTTTATTAATGATGATGTTTTCGATGTTTGTGTTTGT 8769  
Qy 787 ATTTTAAAGACTAGTTGGCAACCTGTTCTTTCAAGATTTGATTTTTCAAA 846  
Db 8770 ATTGTAGTTAAAGAAAGTATTTGTTTGGATTTGTAATTTTATTTTATTTTGA 8829  
Qy 847 AAAATAGTTATTTT 863  
Db 8830 TAAAGTTTATTTTGT 8846

RESULT 3  
US-10-330-773-534  
Sequence 534, Application US/10330773  
Publication No. US20060040262A1  
GENERAL INFORMATION:  
APPLICANT: David W. Morris  
APPLICANT: Marc Malandro  
TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
FILE REFERENCE: 529452001300  
CURRENT APPLICATION NUMBER: US/10/330.773  
PRIOR FILING DATE: 2002-12-27  
NUMBER OF SEQ ID NOS: 981  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 534  
LENGTH: 254396  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-330-773-534

Query Match 4.2%; Score 55.6; DB 7; Length 254396;  
Best Local Similarity 46.2%; Pred. No. 3.3;  
Matches 184; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

Qy 452 AAAAAATTAACCAAGTAACTAATCCACTGAAAGCTATCATGTATGTTTAAAGAAACA 511  
Db 201251 AAGAAAAAAGAAAAAGAAAAAGAGAGAGGAAAGAAAAAGAAAAAGAAAAAGGA 201310  
Qy 512 TCTATTAACCAAGTAACTAATCCACTGAAAGCTATCATGTATGTTTAAAGAAACA 571  
Db 201311 AAGAAAAAAGAAAAAGAAAAAGAGAGAGGAAAGAAAAAGAAAAAGAAAAAGGA 201370  
Qy 572 ACAATTACAAACATCTAAGAGCAGCAAAATTAATCGAAAGTAAGCTATGAGTTTCAGA 631  
Db 201371 GCTGCTCGAATTTTATGACATTAATTTATCTTACCTGCAACATCAAGTTTCATG 201430  
Qy 632 TTTTCTTTTCACTCTGTTATTTGTTATTTGTTTATATATATTTCTTCTTTACA 691  
Db 201431 TTTATCTTTTAAATTTTATTTACATTTATTAATTTATTAATTAATGACTTTT 201490  
Qy 692 ATGAGTGAATTTTCTCCGATTTTATTAATGACTAATGACTATTTTATTAAGCA 751  
Db 201491 AACTGGGGTTTTTTTTTTCAGCAACTTAATTAAGAAAGTCAAGCTTACTACAGCA 201550  
Qy 752 CGCATGCTAGATTTCTGTTCAAAAATCTTCTGATTTTATTAAGAGTAGTTGCGAA 811  
Db 201551 AGAATCAATGCGATTTGATTTAGAACAACTTCAATCATCGGAGTATTTTCTAT 201610  
Qy 812 CCTGTTTCTTCAAGAAATTTGATTTTTCAAAAA 849  
Db 201611 TTGTCAATATTTGTAATCATTTTGTGCTTTTAAAAA 201648

RESULT 4  
US-09-925-065A-54272  
Sequence 54272, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925.065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 54272  
LENGTH: 915  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-54272

Query Match 4.2%; Score 54.8; DB 6; Length 915;  
Best Local Similarity 51.0%; Pred. No. 1.2;  
Matches 151; Conservative 1; Mismatches 143; Indels 1; Gaps 1;

QY 596 ACAAATTATACGAAAGTAGCTAGCTGAGATTTCTTTTCATTCCTGTTAT 655  
DB 347 AAAGATCTATATATATATATATATATATATATATATATATATATAT 406  
QY 656 TTGTTATGTTTATATATATATATATATATATATATATATATATATAT 714  
DB 407 AT 466  
QY 715 TATTAAGCTATTAAGCTATTTATATATATATATATATATATATATAT 774  
DB 467 TATTAAT 526  
QY 775 AAAATCTTCTGATTTTATAGAGCTAGTGGCAACCTGTTCTTCAAGAAAT 834  
DB 527 TAT 586  
QY 835 GATTTTCAAAAAATAGTTATTTCTTTATTAATTAAGAAACCTTAGA 890  
DB 587 TATTTTAT 642

## RESULT 5

US-09-925-065A-803046  
Sequence 803046, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 803046  
LENGTH: 488  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-803046

Query Match 4.1%; Score 53.6; DB 6; Length 488;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
Matches 137; Conservative 1; Mismatches 140; Indels 0; Gaps 0;

QY 610 AAGTAAGCTATGACCTGAGATTTCTTTTCATTCCTGATTTGTTATGTTT 669  
DB 37 ATGACATGTCAGACCTTTGATTTGTTGGAACATCCTTTCTTTTAAACACGTTA 96  
QY 670 ATATACATTTCTTCTTCAATAGAGATTTTCTCGATTTTATTAATAGACTATA 729

DB 97 TTTTATTTAGACTAACTACTACACAGATTTCTTATATATATATATCTCT 156  
QY 730 AGGTATTTTATATATAGACGACGATGCGATATCTGTCGTAATCTTCTGAT 789  
DB 157 TAACTCTTTTACCTCAAAAACCTCTTTCAGAACTTCTTACATTTTATATTC 216  
QY 790 TTTTAAAGCTATGTTGGCAACCTGTTCTTTCGAAAGATTTGATTTTCAAAAA 849  
DB 217 CTGGTCCCTTACCTTCTGTTTATATATATATATATATATATATATATAT 276  
QY 850 AATGATTTATTTCTCTTTATTAATTAAGAAACACTT 887  
DB 277 TGTCTCTTTTCTTTTCTTTTATTAAGAAACACTT 314

## RESULT 6

US-10-240-708-73/c  
Sequence 73, Application US/10240708  
Publication No. US20050282157A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
FILE REFERENCE: 5013.1012  
CURRENT APPLICATION NUMBER: US/10/240,708  
PRIOR FILING DATE: 2002-10-03  
PRIOR APPLICATION NUMBER: PCT/EP01/03971  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: DE 10019058.8  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 96  
SEQ ID NO 73  
LENGTH: 5152  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-240-708-73

Query Match 4.1%; Score 53.6; DB 8; Length 5152;  
Best Local Similarity 48.2%; Pred. No. 3;  
Matches 219; Conservative 0; Mismatches 224; Indels 11; Gaps 2;

QY 425 CATTGGCACTACCGACGAAAGTTTAAAAATTAACCAAGTACTATTCACCTCGA 484  
DB 4137 CTACATCTCCACTCACTCAAAATCTCAACAAAAATTAACCTTAACCCAAATTCGA 4078  
QY 485 AACTATCATGTATATGTTTAAAGAAACATATTAACCAACGATCTCTTAAAAACAAG 544  
DB 4077 AACTATCATTAACCCGTAATTTACGCACTACATTTCAACCTTAACCAAAAAACCTTA 4018  
QY 545 CATATTTGAAAGACAAATTAATGTTACGTTTACAAACATCTAAGAGGACAAATAT 604  
DB 4017 TCTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3958  
QY 605 ATCGAAAGTACATGACCTGACATTTCTTTTCATTCCTGATTTGTTATG 664  
DB 3957 TATATCTAT 3898  
QY 665 TTTTAT 723  
DB 3897 TATTTTAAATTTTACCTTATTTTAAATTAATTAATTAATTAATTAATTAATTAACG 3838  
QY 724 ACTATTAAGCTATTTTATATTAAGAGCAGATGCTGATTTCTGTTCAAAATCTT 783

Db 3837 AACATAAATCAATTTCTTAACACC-----TAAATTAAAAATAAAAAATAT 3788  
Qy 784 CTGATTTTAAAGAGTAGTTGGCAACCGTCTTCTTCAAGAAATTTGATTTTTC 843  
Db 3787 TTCTATTAACATAATTCCTTTAACAACATCTTAATTAATAAATTTTCCATTTT 3728  
Qy 844 AAAAAAATAGTTTATTTTCTCTTAATAATA 877  
Db 3727 AAAAAAATTCCTAAATACCTAAATATTAATAA 3694

## RESULT 7

US-10-240-708-63  
; Sequence 63, Application US/10240708  
; Publication No. US20050282157A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/240,708  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 63  
; LENGTH: 5562  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically created genomic DNA (Homo sapiens)  
US-10-240-708-63

Query Match 4.1%; Score 53.4; DB 8; Length 5562;  
Best Local Similarity 52.4%; Pred. No. 3.3;  
Matches 140; Conservative 0; Mismatches 126; Indels 1; Gaps 1;

Qy 614 TAACCTATGACGTTGATTTTCTTTTCAATCTGTTATTTGTTATTTATAT 673  
Db 1325 TTATATTTTAAGTTATTTATTTTGTGGGGGATTTTGTGTTTTTTTA 1384  
Qy 674 ACATTTCTCTCTTACAATAGAGATTTCTCCGATTTTAATAAGTAAAGT 733  
Db 1385 TTATTTTAATATTTATTTATTTTGTGTTGAGTAAATGATTTTGTGAT 1444  
Qy 734 CATTTTATATAAGCAGCATGTCGATTCGTTCAAAATC-TTCTGATTTT 792  
Db 1445 TATATTTATATTTTATTTTATTTAGTTAGTTTGTGTTTATTTATTTATTT 1504  
Qy 793 TTAAGAGCTAGTTGGCAACCGTCTTCTTCAAGAAATTTGATTTTCAAAAAAT 852  
Db 1505 TTTATTTTGTAGTTAGATTTTGTGTTTATTTATTTTGTGTTTATAGTGT 1564  
Qy 853 TAGTTATTTTCTCTTTAATAATGA 879  
Db 1565 TTTTATTTTGTGTTAAGAA 1591

RESULT 8  
US-10-995-561-13314/C  
; Sequence 13314, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: C0001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13314  
; LENGTH: 119036  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1) ..(119036)  
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-7)  
US-10-995-561-13314

Query Match 4.1%; Score 53.2; DB 8; Length 119036;  
Best Local Similarity 48.4%; Pred. No. 7.4;  
Matches 177; Conservative 0; Mismatches 188; Indels 1; Gaps 1;

Qy 619 TAAGCGTTCAGATTTTCTTTTCAATCTGTTATTTGTTATTTGTTATATATAT 678  
Db 31623 TAAATCTTATTTTATATATTTTATATATTTTATATATATATATATATATA 31564  
Qy 679 TTCTTCTTACATAGATTTTCTCCGATTTTATATAATGACTAATAGTCAATT 738  
Db 31563 TTTTATATATATAAATTCATATTTTATATATTTTATATATTTTATATATGAAATC 31504  
Qy 739 TTAATATAAGCAGCATGTCGATTCGTTCAAAATCTTCTGATTTTATAGA 798  
Db 31503 TTATTTATATATATTTTATATATTTTATATATATATATAAATCTTATATATATA 31444  
Qy 799 GCTAGTTGGCAACCGT-TTCTTCAAGAAATTTGATTTTTCAAAAAATAGTT 857  
Db 31443 TTTTATATATATATAAATCTTATTTTATATATATTTTATATATATAAATCTTATTT 31384  
Qy 858 TATTTCTCTTAAATAGAAACACTAGAAATAGAGTTGCCAGTACCTAG 917  
Db 31383 TATATATTTTATATATATATATAAATCTTATTTTATATATTTTATATATATAA 31324  
Qy 918 AATGTTTCCCAATTAATCAATCACTGTTATATTTATTTGGCCAGCCCAATTA 977  
Db 31323 TCTATTTTATATATATTTATATATATATATATAAATCTTATTTATACGCAATTTCTAA 31264  
Qy 978 TTTAAA 983  
Db 31263 ATAAAA 31258

RESULT 9  
US-09-925-065A-803045  
; Sequence 803045, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09



Db 61557 ATATATATATGTCACATATATATTTTATATATATATATATGACATATATATTTTATAT 61498  
 QY 743 ATAGAGCAGCATGTCGTGATTCGTTCAAAAACTTCTGATTTTTTAAAGCTA 802  
 Db 61497 ATATATATATGTCACATATATATTTTATGATATATATGATATATATATTTTATGATAT 61438  
 QY 803 GTTGGCAACCGTTTCTTTCGAAGATTTGATTTTTTCAAAAAATAGTTATTT 862  
 Db 61437 ATATATATTTTATGATATATATATATTTTATCGATATTTTATATATATATATATTTT 61378  
 QY 863 TCTCTTATATAATAGAAAAACCTGAGAAAAATAGAGT 900  
 Db 61377 TATATATATATATATACATTTTATATATATATATATAT 61340

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RESULT 12
US-11-121-086-25
: Sequence 25, Application US/11/121.086
: Publication No. US2005026659A1
: GENERAL INFORMATION:
: APPLICANT: POULSEN, TIM S
: APPLICANT: NIELSEN, KIRSTEN V.
: TITLE OF INVENTION: NOCLETIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
: FILE REFERENCE: 09138, 6000-00000
: CURRENT APPLICATION NUMBER: US/11/121.086
: PRIOR FILING DATE: 2005-05-04
: PRIOR APPLICATION NUMBER: 60/567,570
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 25
: LENGTH: 173602
: TYPE: DNA
: ORGANISM: Homo sapiens
US-11-121-086-25

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Query Match	3.9%	Score	51.4	DB	12	Length	173602
Best Local Similarity	45.5%	Pred. No.	17				
Matches 219, Conservative	0	Mismatches	261			Indels	1
						Gaps	1

[illegible]

QY	954	T	954
Db	137018	T	137018

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RESULT 13
US-10-330-773-26
; Sequence 26, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; PTL REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 687411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(687411)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-26

```

Query Match	3.9%	Score 51.2;	DB 7;	Length 687411;
Best Local Similarity	46.2%;	Pred. No. 25;		
Matches 170;	Conservative 0;	Mismatches 198;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 14
US-09-925-065A-667262
; Sequence 667262, Application US/09925065A
; Publication No. US2004018104B1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleoside Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096

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PRIOR FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: US 60/252,147  
 PRIOR FILING DATE: 2000-11-20  
 PRIOR APPLICATION NUMBER: US 60/250,092  
 PRIOR FILING DATE: 2000-11-30  
 PRIOR APPLICATION NUMBER: US 60/261,766  
 PRIOR FILING DATE: 2001-01-16  
 PRIOR APPLICATION NUMBER: US 60/289,846  
 PRIOR FILING DATE: 2001-05-09  
 NUMBER OF SEQ ID NOS: 957086  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 667262  
 LENGTH: 677  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-925-065A-667262

Query Match 3.9%; Score 51; DB 6; Length 677;  
 Best Local Similarity 45.6%; Pred. No. 5.4;  
 Matches 214; Conservative 1; Mismatches 251; Indels 3; Gaps 1;

492 ATGTAATGTTTAAAGAAACATCTATTAAACCGACATCCTCTTAAACAAAGCATATTT 551  
 31 AT 90  
 552 CGAAGAGCAAT 611  
 91 AT 150  
 612 GGTACGCTATGACGTTGACATTTCTTCTTCAATGTTGTTATTTGTTAT 671  
 151 TATATAAT 210  
 672 ATACATTTCTTCTTCAATGTTGTTATTTCTTCAATGTTGTTATTTAT 728  
 211 AT 270  
 729 AAAGTCATTTTAT 788  
 271 AT 330  
 789 TTTTAAAGCTAGTTGGCAACCGTCTTCTTCAAGATTTGATTTTCAAAAA 848  
 331 TATTATGAT 390  
 849 AAATGATTTATTTCTTCTTCAATGTTGTTATTTCTTCAATGTTGTTATTT 908  
 391 TAT 450  
 909 TAGCCCTAGATGTTTCCCATATATATATATATATATATATATATATATATATAT 957  
 451 AAT 499

RESULT 15  
 US-09-925-065A-667263  
 Sequence 667263, Application US/09925065A  
 Publication No. US20040181048A1  
 GENERAL INFORMATION:  
 APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single  
 Nucleotide Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827.135  
 CURRENT APPLICATION NUMBER: US/09/925,065A  
 PRIOR APPLICATION NUMBER: US 60/243,096  
 PRIOR FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: US 60/252,147  
 PRIOR FILING DATE: 2000-11-20  
 PRIOR APPLICATION NUMBER: US 60/250,092  
 PRIOR FILING DATE: 2000-11-30  
 PRIOR APPLICATION NUMBER: US 60/261,766  
 PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846  
 PRIOR FILING DATE: 2001-05-09  
 NUMBER OF SEQ ID NOS: 957086  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 667263  
 LENGTH: 677  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-925-065A-667263

Query Match 3.9%; Score 51; DB 6; Length 677;  
 Best Local Similarity 45.6%; Pred. No. 5.4;  
 Matches 214; Conservative 1; Mismatches 251; Indels 3; Gaps 1;

492 ATGTAATGTTTAAAGAAACATCTATTAAACCGACATCCTCTTAAACAAAGCATATTT 551  
 31 AT 90  
 552 CGAAGAGCAAT 611  
 91 AT 150  
 612 GGTACGCTATGACGTTGACATTTCTTCTTCAATGTTGTTATTTGTTAT 671  
 151 TATATAAT 210  
 672 ATACATTTCTTCTTCAATGTTGTTATTTCTTCAATGTTGTTATTTAT 728  
 211 AT 270  
 729 AAAGTCATTTTAT 788  
 271 AT 330  
 789 TTTTAAAGCTAGTTGGCAACCGTCTTCTTCAAGATTTGATTTTCAAAAA 848  
 331 TATTATGAT 390  
 849 AAATGATTTATTTCTTCTTCAATGTTGTTATTTCTTCAATGTTGTTATTT 908  
 391 TAT 450  
 909 TAGCCCTAGATGTTTCCCATATATATATATATATATATATATATATATATATAT 957  
 451 AAT 499

Search completed: March 6, 2006, 10:32:43  
 Job time: 1372.54 secs

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